

Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:10:02 ; Search time 49 Seconds

(without alignments)

5634.254 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTLTATEQPVKNTLKK.....QPVSEILQLKTYLPPFETI 875

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPTREMBL 25::*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriop:*

17: sp_archeap:*

ALIGNMENTS

RESULT 1

Q99KC7 PRELIMINARY; ID Q99KC7; AC Q99KC7; DT 01-JUN-2001 (TREMBLrel. 17, Created); DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update); DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update); DE Similar to eucocneotide pyrophosphatase/phosphodiesterase 3 (Fragment).

Q17540 caenorhabditis

Q22129 caenorhabditis

Q8719 xylolela fas

Q94K08 rabidopsis

Q96m57 homo sapien

Q98bgn3 mus musculus

Q8718 homo sapien

Q9778 listeria mo

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	2540_5	52.9	565	11	Q99KC7	Q99KC7 mus musculus
2	2415	50.7	906	11	Q924C4	Q924C4 mus musculus
3	2191	45.6	874	13	Q7ZRN7	Q7ZRN7 xenopus lae
4	1360	28.3	251	4	Q9NQ9	Q9NQ9 homo sapien
5	1263	26.3	817	12	Q9JTH1	Q9JTH1 fowlpox vir
6	1263	26.3	817	12	09761	09761 fowlpox vir
7	972	20.2	415	11	Q8CAF0	Q8CAF0 mus musculus
8	837	17.4	195	11	Q9IVZ7	Q9IVZ7 mus musculus
9	835	17.4	152	4	Q9HS15	Q9HS15 homo sapien
10	755.5	15.7	479	10	Q9FS13	Q9FS13 spinacia ol
11	746	15.5	274	4	Q723P5	Q723P5 homo sapien
12	743.5	15.5	496	10	Q9SU83	Q9SU83 arabidopsis
13	737.5	15.4	479	10	Q42774	Q42774 oryza sativ
14	713.5	14.9	457	10	Q84WJ3	Q84WJ3 arabidopsis
15	712.5	14.8	457	10	Q9SU82	Q9SU82 arabidopsis
16	680.5	14.2	461	10	Q9SU81	Q9SU81 arabidopsis

SEQUENCE FROM N.A.

RP STRAUBERG R.; RA

RL SUBMITTED (MAR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC005527; AA05527; 1; -.

DR MGI; MGJ:2143702; Engp3.

DR GO; GO:0004519; F:Endonuclease activity; IEA.

DR GO; GO:0016787; F:Hydrolyase activity; IEA.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR001604; Endonuclease.

DR Pfam; PF01223; Endonuclease; 1.

DR SMART; SM00477; NUC; 1.

DR NCBITaxon; NCBI TAXID=10990; 1.

DR SEQUENCE 565 AA; 63895 MW; 7179104P1863A04 CRC64;

Query Match 52.9%; Score 2540.5; DB 11; Length 565;

Best Local Similarity 81.1%; Pred. No. 3.1e-207; Matches 53; Mismatches 51; Indels 3; Gaps 3;

Matches 460; Conservative 53; Non-Conservative 459; Gaps 3;

Qy 310 KAERPFYTMVFEPPDSGHAGGPYSARTVKAQYDHAEGMGLMEGLKORNLNQVNII 369

Dy 1 KADPSPYTYEEEDSAGHSGPVSGVTKAQVDNAGMMEGLKORNLNQVNII 60

SQ	SEQUENCE	906 AA;	103125 MW;	1PA071071E4B950	CRC64;
Qy			Query Match	50.7%;	Score 2435;
			Best Local Similarity	51.0%;	DB 11; Length 906;
			Pred. No.	5.8e-198;	
			Matches	447;	Conservative 152; Mismatches 250;
Db			Q8PVKCK-----NTLKKYKIACTVLLAVLIVSGLGLGLRKLEQGSKRKCF	5.9	
Db			39 EEELEKAERAPAKDPTT--YKVLSSLVSYCVLTLGICFGLKPSCAKEVKSRGRCF	9.5	
Qy			60 DASFRGLENCRCDVACKDRGDCWDFDDTCVESTRWMNKRPGTRLEASLCSGDDC	1.19	
Db			96 ERTF--SNCRCDAACTSYLGNCLDFOETCYBPTHTWTCNPRCGBKLRSFVCSADD	15.2	
Qy			120 LQKDDCCADYKSVCGTSWLBENCHTAQQSOCCEGFDLPPVTLFSMDGFRAEYLTYWDT	1.79	
Db			153 KTHNDCCINYSSVQDKKSWVEETCSIDTPECAFEESPPTLFLSDGFRAEYLHTWGG	21.2	
Qy			180 IMPNTINLKLTKTCIHSYCMRATYPTKTFPPNHTTIVTGHYPERSGHIIIDNMYDNLNQFSL	2.39	
Db			213 LPVPSVJKNQCTYTMNRMPTKTFPPNHSIVTGHYPERSGHIIIDNMYDNLNQFSL	2.72	
Qy			240 SSKEQINQPAMWGGQPKWLTAMYQKHLKATYFPGSEBVAINGSPSPSYMPYNGSVPPFEERI	2.99	
Db			273 XSKEKINPLWYKQQPWVTAHQEVSGTGYWPGSVEIDGILPDYKTVNGSVPPFEERI	3.32	
Qy			300 STLLKNLDLPAERPFYTMFEPPSSGHAGGPYSARVIAKQVDFHARFGLMELPKQR	3.59	
Db			333 LAVLENQLPSPHERPFYTYLEEPSSGHSHGPYSESEVIKALQKVDRLYGMLMDLQKDL	3.92	
Qy			360 NHNCVNTILLADHGMDQTYCNKMEYMTDYPRTINFYMEGPAPIRAINLPHDFDSFN	4.18	
Db			393 GLDKCMLNLISDHGNEQGSCSKRTVNLNQFLGDNVNTKVVGPAAELRPTDVPTVFSN	4.52	
Qy			420 SEEIVRNLSCKPDKHFKPVLTPDLPKRLHYAKVNDKVKLFLVDQWQ-LAVRSKNTNC	4.78	
Db			453 YEALAKNLSCKEPNQFRPYKJPLPRLHAKSDIEPLTFYDQWQALNPSRSRYC	5.12	
Qy			479 GGGNHGYNNEFRSMELIELAHGPSKEKETVBPENIEXXNLMCDLRLIQAPANNGTHG	5.38	
Db			513 GSGFROSNDNLNQMLQFQGPAFHGAEVDSFENIEVNLMCGLGLQPAKNSCHG	5.72	
Qy			539 INHLKCFPTEPSSHAEVRSKSVCGANPLDTECFCPHLQNSQLEQNQMLNLTQ	5.98	
Db			573 INHLKCFPTEPSSHAEVRSKSVCGANPLDTECFCPHLQNSQLEQNQMLNLTQ	5.98	
Qy			599 BITATVNLDFGRPVLQKRNVDHCLLYHREYVSGGRKANRMPMWSYTYPQLGDTSPPL	6.58	
Db			629 DVDDDIKMTTFYGRPILLKQHRLPAQQLFQFLTSDMLIMPWASYTF-LSDNQFSR	6.86	
Qy			659 PTVPDCLRADYRVPPEQSOKCSFYLADKNFTHGFLYPPASNRTSDQ-YDALITSNLVP	7.17	
Db			687 DDFSNSLQYQDRIPLSPVACSYNSNSKSYGFITPRLNRSVHISYSEALTSNIVPM	7.46	
Qy			718 YEEFRKMDYFHSVLLIKHATERGUNVNSGPIEDYNGDGHEDADDBITKH--LANTDV	7.74	
Db			747 YQSFQVIMHTLHDITLQRYAHERGNGVNSGPVFEDYDGRYDSLIEILKNSRVSRSQE	8.06	
Qy			775 PIPTHYFWVLTSCKNSHTPENCPGMWLDVLPFPIIHRPRTIVNECPCBGPBALWTEBFRTA	8.34	
Db			807 LIPHTIFFIVTSCQKOLESETLECSA-LESSAYILPHRPDNESTCHGKRESSYVEELTL	8.65	
Qy			835 HIARYRDVELTGLDQYODKVPQYSBLLQKRTYLPF	8.71	
Db			866 HRARVTDVELTGLSFYQDRQESVSELLRKLTHLPF	9.02	
	RESULT 3				
	Q7ZKXN7				
	ID				
	Q7ZKXN7;				
	AC				
	01-JUN-2003				
	(TREMBlrel. 24, Created)				
	DT				
	01-JUN-2003				
	(TREMBlrel. 24, Last sequence update)				

DT	01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE	Hypothetical protein
OS	Xenopus laevis (African clawed frog)
OC	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE:Embryo;
RA	Klein S.; Straubberg R.;
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; EMBL; BAA4675; AAH4675; 1; -
DR	GO; GO:0004419; F:endonuclease activity; IEA.
DR	GO; GO:00165787; F:hydrolase activity; IEA.
DR	GO; GO:0003876; F:nucleic acid binding; IEA.
DR	GO; GO:009117; F:nucleotide metabolism; IEA.
DR	InterPro; IPR001604; Endonuclease.
DR	InterPro; IPR002591; Phosphodiester.
DR	InterPro; IPR001212; Somaticoedit.
DR	Pfam; PF0123; Endonuclease; 1.
DR	Pfam; PF01663; Phosphodiester; 1.
DR	Pfam; PF01033; Somaticoedit; 2.
DR	PRINTS; PR00022; SOMATOMEDINB.
DR	SMART; SM00477; NUC; 1.
DR	SMART; SM00301; SC; 2.
DR	SMART; SM00524; SONATOMEDIN_B; 2.
KW	hypothetical protein
SEQUENCE	974 AA; 99650 MW; 7EAB4EC1D9FCE46 CRC64;
SQ	-----
Query Match	45.6% ; Score 2191; DB 13; Length 874;
Best Local Similarity	45.1% ; Pred. No. 3 2e-177;
Matches	409; Conservative 161; Mismatches 255; Indels 82; Gaps 14;
Qy	15 KNTLKKYKIACTYLALIVIMSLIGLGLGK-RK-----
Qy	4 KNGSFHVKVSLVTFAGTCINVLGCFTRKSEENDEGVASVLSDFPWRSSGSKERC 63
Db	59 FDASPRGLENCRDVACKDRGDCWDFEDTCYESTRIMWCNKPRCGBTRELASICSD 118
Db	64 FELJEEAAPACRCDNLCKSYNSCCEDFELHCLKTGREWECIKDRGBTRENEACHCS 123
Qy	179 CLOKKDCADYKRSVCGGTSLBENDCAQGQCPBDFDLPVVLMSMDGPRAEVLYTWD 178
Qy	119 CLOKKDCADYKRSVCGGTSLBENDCAQGQCPBDFDLPVVLMSMDGPRAEVLYTWD 178
Db	124 CLAKGDCTNYQVCKGUTHADDCEBMKHEPCPAGFVRPLIISVDFGRASYMKGH 183
Qy	238 LSSKEQNNPAWNHGQPMWLTAMYQKIAATYFWPGSEVATINGSFPSYMPYNGSYFER 298
Db	244 LREKEFNHRWNGQPIWITASQGLKATFMPWV---VAVSO-----ERR 285
Qy	299 ISTLKLNDLPLKZERPRFTYMFEEPDSGHAGGPVSARVIAKLOVYDHAEGMIMBGLKQ 358
Db	286 IFTVLOWHNDPDERPRTYALYSEQDQAGHXYGPQFQELAEQKLYNDKIVGQLMGLKQ 345
Qy	359 RNEHNCVILLADHGQWQTYCNKMEYTDIYPRINFINYMEGAPRIRAH-1-PHDFF 416
Db	346 MKLHRCVNVIFVGDHGMEEATCERTEFLNSVNVDDFALLPGSIGRSRNPNKHD-- 403
Qy	417 SFNSEEIVRNLSCKPDKDHFKPYLPDPLKPRHYAKNVRIDKVLFDQWMLAVRS--- 472
Db	404 ---PKAVIANTLCKPKDHFKPYLPDPLKPRHYAKNVRIDKVLFDQWMLAVRS--- 460
Qy	473 -KSNTNCGC-GGNHGYNNFRSMEAFLPHGPFSEKEKTEVEPPENIEVYNLMCDLJLRIQAP 530
Db	461 YKRGQKCAFQGDHYDNKITSMQLVFLGPSPKTYKXVPPFENIEVNMCDLJLRIQAP 520
Qy	531 PNTGTHGSNLHLLKVPFEPKSHAEVSKESVCGFANPLP-----TESLDCFCPHLN 582
Db	521 SNNTHGGSNLHLLRVA\$KPAIPDEVSK-----PLPVTSPTVNEELGSC---DD 569
Qy	583 STQLEQVNQML-----NLTQBEETATVK-----VNLPGFRPRVYQKNVYDHCLLYHR 628
Db	570 KNAEELNRLYIGKTGTDVAEELSEKELTSRNTDNLGTRKLYHJHS 628
Qy	629 EYVSGFGKAMRMWNKSSYTVPOQGDTSPLUPPTVPODCLRADYVPPSESQKCSFYLLADKNI 688
Db	629 DFEFGSESLQMPWMTSITSKQADVSCEHESNCVRLDPRISPGNSQCSAYKADQMQ 688
Qy	689 TKGLYPPASNRTSDSQDALISNLVYMEERKMDYFHSVLLKHTERNGNTVSG 748
Db	689 SYGFLPPQLOSSADSQVDAFLTNVPLYPAFKKNNYFORVLCRPEATERGVNTVSG 746
Qy	749 P1PD2YD9SHFDEDEITKHLANTDVPPTPHYFVVLTSCKNSHTPENCPGWLDDVLPLII 808
Db	749 P1PD2YD9WYDPMK1-KMFDGSIPIPPTHYYIISCMDNQAVNCDGCLSVSVSTV 807
Qy	809 PHRPINVECPGKPEALWEEERTHAIARVDRDVEELITGLDFYQDVSEILQLQTYL 868
Db	808 PHRPDNEDESNSBESKVNEDLKLKHTTRDIELLTGLDFYRKTNRSYTEILSLKTYL 867
Qy	869 PTEFTLI 875
Db	868 HTYESEI 874
RESULT 4	
Q9NQ9	Q9NQ9 PRELIMINARY; PRT; 251 AA.
ID	Q9NQ9 ID Q9NQ9
AC	Q9NQ9; AC
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB	DJ105H11.3 (Phosphodiesterase I/nucleotide pyrophosphatase 3) (Fragment).
DB	DN1M1.1 (Fragment).
GN	Home sapiens (Human)
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; NCBI_TaxID=9606;
OC	
OC	
OX	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Lovell J.;
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; ALJ35904; CAB99214.1; -
DR	GO; GO:0004510; Endonuclease activity; IEA.
DR	GO; GO:0003676; Nucleic acid binding; IEA.
DR	GO; GO:0009117; Nucleotide metabolism; IEA.
DR	InterPro; IPR002591; Endonuclease.
DR	InterPro; IPR002591; Phosphodiester.
PFam	PF01663; Phosphodiester; 1.
DR	SMART; SM00477; NUC; 1.
FT	NON_TER 1
FT	SEQUENCE 251 AA; 28225 MW; C726FD4719D4880C CRC64;
FT	NON_TER 1
FT	SEQUENCE 251 AA; 28225 MW; C726FD4719D4880C CRC64;
Query Match	28.3%; Score 1360; DB 4; Length 251;
Best Local Similarity	100.0%; Pred. No. 2 1e-10; Nuc; 0; Indels 0; Gaps 0;
Matches	251; Conservative 0; Mismatches 0;
Qy	472 SKSNTNCGGNGHGYNNFRSMEAFLAHPSEKEKTEVEPPENIEVYNLMCDLJLRIQAP 531
Db	1 SKSNTNCGGNGHGYNNFRSMEAFLAHPSEKEKTEVEPPENIEVYNLMCDLJLRIQAP 60
Qy	532 NNGTGSNLHLLKVPFEPKSHAEVSKFSVCGFANPLPESLDFCPHLQNSTQLEQVQ 591
Db	61 NNGTGSNLHLLKVPFEPKSHAEVSKFSVCGFANPLPESLDFCPHLQNSTQLEQVQ 120
Qy	592 MLNLTQEEITATVKNLPPGRPRVYQVNDHCLLYHREVSFGFARMNPMSYTVQL 651
Db	121 MLNLTQEEITATVKNLPPGRPRVYQVNDHCLLYHREVSFGFARMNPMSYTVQL 180

Qy	652 GDTSPPLPPTVDPCLRADYRVPPESEOKCSFYLADKNITHGFLYPPASNRTSFSDSYDALIT 711	Db	465 RVPIFDNIELYNMCEILGINPANNNGTVGSILNLNSRY -THVSLDITI----- 516
Db	181 GDTSPPLPPTVDPCLRADYRVPPESEOKCSFYLADKNITHGFLYPPASNRTSFSDSYDALIT 240	Qy	568 LPTESSLDC-----FCPHQNSTOLBQVNQMLNLTQBBITAVK---VNLPFGPRPVHQ 617
Qy	712 SNLVPMPTEFR 722	Db	517 ---ES-ECDRAHYGDHLKGCT-CKN1DRFSSKGKNDSSRTRSSYYTINULPGKAVLL 571
Db	241 SNLVPMPTEFR 251	Qy	618 KNDVHCLLYHRETVSGFGRAMNPWSSYTVP-QLGTSPLPLPTVDCRLADVRVPSES 676
RESULT 5		Db	572 NRHHHC1IKNDNVTATSKVNLPLWTSFSTDITYTNLYNKT---CYLQDMRV-MYYK 627
Q9J5H1	PRELIMINARY;	PRT;	817 AA.
ID	Q9J5H1/		
AC	AC_09J5H1_		
DT	DT_01-OCT-2000 (TREMBrel. 15, Created)	Qy	677 QKCSFSYFLADKNITHGFLYPPASNRTSFSDSYDALITSNLVPMEEFKRMWDYHSVLLKH 736
DT	DT_01-OCT-2000 (TREMBrel. 15, Last sequence update)	Db	628 EPCRYSTSKQDVTGILYPA--RATD-FQSILETTVPMFNRKIIWEFMSSLLIEY 682
DT	DT_01-OCT-2003 (TREMBrel. 25, Last annotation update)	Qy	737 ATERNGNNVNSGPIFDYNDGHDADPDBTKHLA-NTDVP1PHTHYTVLTVLTSCKNKSHTPE 795
GN	GN_FPV030 alkaline phosphodiesterase.	Db	683 VQKHVVNVMVGFEDNSNG1RDSDFLMSGSYNNKVVIFPSDVFVILYCKDKDSLNL 742
OS	OS_Fowlpox virus (FPV).	Qy	796 NCPCWLDLVPFLPIPHRTNV-ESCP-BGKPEALWVEERFTIAHARYDVELLTGLDFYQD 853
OC	OC dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;	Db	743 DCYSNKITESFVVPNSPTTYNNESCSRERNITSVSYVRFKFLSLHRVRIKDIETVTSMSFYRN 802
OX	OX NCBI_TaxID=10261;	Qy	854 KIVOPVSEELQQLKTYL 868
RN	RN_	Db	803 VYKTSNNTAVLKYM 817
RP	RP_SEQUENCE FROM N.A.	RESULT 6	
RX	RX_MEDLINE=20193820; PubMed=10729156;	Qy	090761 PRELIMINARY; PRT; 817 AA.
RA	RA_Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;	AC	090761; PRELIMINARY; PRT; 817 AA.
RA	RA_SEQUENCE FROM N.A.	DT	01-NOV-1998 (TREMBrel. 08, Created)
RA	RA_Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	DT	01-NOV-1998 (TREMBrel. 08, Last sequence update)
RA	RA_EMBL; AF198100; AA#4374.1; -	DR	01-OCT-2003 (TREMBrel. 25, Last annotation update)
DR	DR_GO: GO:0016519; F:endonuclease activity; IEA.	DE	Alkaline phosphodiesterase I (EC 3.1.4.1).
DR	DR_GO: GO:0016787; F:hydrodase activity; IEA.	GN	PC1.
DR	DR_GO: GO:003676; F:nucleic acid binding; IEA.	OS	Fowlpox virus (FPV).
DR	DR_GO: GO:009117; P:nucleotide metabolism; IEA.	OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
DR	DR_InterPro: IPR001604; Endonuclease.	OC	Avipoxvirus.
DR	DR_InterPro: IPR000591; Phosphodiest.	OX	OC viruses.
DR	DR_Pfam: PF01663; Phosphodiest; 1.	RN	NCBI_TaxID=10261;
DR	DR_SMART: SM00477; NUC; 1;	RP	SEQUENCE FROM N.A.
SQ	SQ_SEQUENCE 817 AA; 94038 MW; 8404FD00641DA022 CRC64;	RC	STRAIN=FP-9;
		RX	MEDLINE=98-35194; PubMed=9658122;
		RA	Laidlaw S.M., Anwar M.A., Thomas W., Green P., Shaw K., Skinner M.A.;
		RT	RT_Poivpox virus encodes non-essential homologs of cellular alpha-SNAP, PC-1 and an orphan human homolog of a secreted nematode protein.";
		RL	RL_J. Virol. 72:6792-6795 (1998).
		DR	DR_EMBL; AJ000408; CAA07014.1; -
		DR	DR_GO; GO:0004519; F:endonuclease activity; IEA.
		DR	DR_GO; GO:0016787; F:hydrodase activity; IEA.
		DR	DR_GO; GO:003676; F:nucleic acid binding; IEA.
		DR	DR_GO; GO:0004528; F:phosphodiesterase I activity; IEA.
		DR	DR_InterPro: IPR001604; Endonuclease.
		DR	DR_InterPro: IPR005591; Phosphodiest.
		DR	DR_Pfam: PF01663; Phosphodiest; 1.
		DR	DR_SMART: SM00477; NUC; 1.
		SQ	SEQUENCE 817 AA; 94004 MW; CB69DA0508CC568E CRC64;
			Query Match 26.3%; Score 1263; DB 12; Length 817;
			Best Local Similarity 36.9%; Pred. No. 2.6e-98; Gaps 18;
			Matches 271; Conservative 145; Mismatches 279; Indels 40;
Qy	149 QSQCPPEFDLPPVILFMDGFRAYLTWDTLMPNINKLKTGITHSKYKAMYPTKTFEN 208	Qy	149 QSQCPPEFDLPPVILFMDGFRAYLTWDTLMPNINKLKTGITHSKYKAMYPTKTFEN 208
Db	108 QVTCPPPERPLILAMNGPDRYDINKWKEVYIPTKDLMEHGTVTAP-KRPVYPTNTEN 166	Db	108 QVTCPPPERPLILAMNGPDRYDINKWKEVYIPTKDLMEHGTVTAP-KRPVYPTNTEN 166
Qy	209 HYITVGLYPESHGIDNQNNDVNLNKNFSSKSEQQNPPAWHGOPMULTAMYOGLKAAT 268	Qy	209 HYITVGLYPESHGIDNQNNDVNLNKNFSSKSEQQNPPAWHGOPMULTAMYOGLKAAT 268
Db	167 LYSITVGLYPISHGTTNEIDRGTIEFTIASEETEEVWEGGPINTWIMQNGFKSAT 226	Db	167 LYSITVGLYPISHGTTNEIDRGTIEFTIASEETEEVWEGGPINTWIMQNGFKSAT 226
Qy	269 YWPGESEVINGSFPTIYMPNGSUFPEERFISTLXWLDPKASRPRFTMYFEPDSSG 328	Qy	269 YWPGESEVINGSFPTIYMPNGSUFPEERFISTLXWLDPKASRPRFTMYFEPDSSG 328
Db	227 FWPFGSDXVPRKRPTYSNKS/ PYEERINTVLRWLXMDQTLGQNLVSDHGMNSVTPKIVNLKD 346	Db	227 FWPFGSDXVPRKRPTYSNKS/ PYEERINTVLRWLXMDQTLGQNLVSDHGMNSVTPKIVNLKD 346
Qy	329 HAGGPVSAVIKALQVVDHAQGMNLEQKQNRLNCVNTILLADHGMDTQYFALYEEPGSSG 286	Qy	329 HAGGPVSAVIKALQVVDHAQGMNLEQKQNRLNCVNTILLADHGMDTQYFALYEEPGSSG 286
Db	287 YEYGTDDERVKALEVDKA1ALMKG1QDQLQIGANLIVSDHGMNSVTPKIVNLKD 346	Db	287 YEYGTDDERVKALEVDKA1ALMKG1QDQLQIGANLIVSDHGMNSVTPKIVNLKD 346
Qy	389 YFPRINFFYMEGPAPIRAHNIPDFFSPNSEEEVTRNLSCRKPDQHFKPLTBDLPKRL 448	Qy	389 YFPRINFFYMEGPAPIRAHNIPDFFSPNSEEEVTRNLSCRKPDQHFKPLTBDLPKRL 448
Db	347 YITN-NDVVKPQGATPKVQNLNH-IRLDYDGIISSITCVMDDQPFVSYSLRPLPRL 404	Db	347 YITN-NDVVKPQGATPKVQNLNH-IRLDYDGIISSITCVMDDQPFVSYSLRPLPRL 404
Qy	449 HYAKNVRIDKVHFLWDQOWLAVRSKSN-TMGGGNHGYNNEFRSMEALFLAHCPSFKEKT 507	Qy	449 HYAKNVRIDKVHFLWDQOWLAVRSKSN-TMGGGNHGYNNEFRSMEALFLAHCPSFKEKT 507
Db	405 HYGSFPTIEVIGVYLBEGWQSTDENGNLKRSGGPHGSDSDFQMTAVLGYGAFLDV 464	Db	405 HYGSFPTIEVIGVYLBEGWQSTDENGNLKRSGGPHGSDSDFQMTAVLGYGAFLDV 464
Qy	508 EVEPFENIEYTNMCDLRLRIOPAPNGTHGSNLHLLKVPFYPESHAEEVSKFWSVGFANP 567	Db	508 EVEPFENIEYTNMCDLRLRIOPAPNGTHGSNLHLLKVPFYPESHAEEVSKFWSVGFANP 567

Qy	2659 YFWPGSEVAINGSFPSITYMPYNGSVPEPERISTLKKWLDLPAERPRFTMYFEEPDSSG	328	DR Pfam; PF01663; Phosphodiester; 1.
Db	2277 FFWGSDKVVPRKPTMVRSTKNSVSPYERINTVRLWLMQDGYRYFAYLLEEFPGSSG	286	DR Pfam; PF01033; Somatomedin_B; 2.
Qy	3229 HAGGPVSSERVITALQWTHAFGMIGMEIGIKQRMILHNQNTILLADHGMQDQTCNKNKEYMTD	388	DR SMART; SMO0201; SO; 2
Db	287 YEGTDDDRVGKALEKVRDIAILMKGKDLQGLIGANLILIVSDHEMSVNDPKKLVNLKD	346	DR PROSITE; PS0024; SOMATOMEDIN_B; 2.
Qy	3889 YFPRINPFTYMEGPAPIRAHNIPHDFFSNBEEIVNLSPRKDPDQHFKPVLTPDLPKRL	448	DR SEQUENCE; 415 AA; BC09A7742C6A3B60 CRC64;
Db	347 YLTN-NDVVIKPEATPVKPKQNLNH-IRLFQDGIISSTSQCMDDQPFIVSYRSRIFKRL	404	Query Match 20.2%; Score 972; DB 11; Length 415;
Qy	449 HYAKNVRDVKHIFLFDQOMLAVRSKSN-TNCGGGHGNHYNNEFRSMBAFLAHGSPFKEKT	507	Best Local Similarity 41.0%; Pred. No. 5.re-74;
Db	405 HYGGSPRTBILGVYLGEBQSTDENGLKHSRGGPHGSNSQDMTAVFELGYGPAPLDDV	464	Matches 172; Conservative 72; Mi smatches 124; Indels 52; Gaps 4;
Qy	508 EYEPFENEVYNNICMDLURIQPAPNNGHGSANLHILKVPFTEPSHAEEVSFKSYVCCFANP	567	Qy 3.2 LIVNSLGLIGLGLG---LRKLE-----KQGSRKCPDASFRGLENCR 70
Db	455 RVPFIDNELYNNCEIIGINPANNINGVGSLNLRNRSY--THVSSLDTITI-----	516	Db 15 LFTFPIGNICLGPATKRAENDEGPPTVLSDSPWNTSGSCKGRCPFLQEVGPPPCR 74
Qy	568 LPTEFLDC-----FCPHLQNSTOLEBQVNQMLNLTQEBITATVK-----VNLPGFGRPRVLF	617	Qy 71 CDVACKDRGBCCMWDEDTCVESTRIMWMCNKFRGCBTRLEASLCSDDCLQEDKCADYK 130
Db	517 ---ES-EDCRHAYGDHKGCH-CKNIDRFSSKGKEDSSRTRSSXYIYLNLPFGPAVIL	571	Db 75 CDNLCKSYSSCCHDDELCKTARGWCTKDRGCEVRENEACHSEDLSRGDCCTNQ 134
Qy	618 KVDHCHLILYHREYSGFEGKAMRMPMMSYTYVP-QLGDTSPLSPPTVPCDLRDAVYPPSES	676	Qy 131 SVCGCETSYLEENCTAQCOSQCPEGFDLPPVILFSMDGFRAYETLTWDTLMPNINKLKTIC 190
Db	572 NRHHHCITKNDNTVTAISKVNRLPLNTFSIDITYNNTNKT---CYLQDMRV-MYK	627	Db 135 VVCRGEBSHWDDCEEIRVPECPAGFVRPLIIFSVGDRASYNKGSKMPNIEKURSC 194
Qy	677 QKCSFYLADKNTTHGFLPPASNRTSISQYDYLTSWLVPMYEERFKMWDYFHSVLLIKH	736	Qy 191 GIHSKSYMRAMYPTKTFPNHYTIVTGYLPESHGHLIDNNMYDNLNKNSLSSKBNQNPW 250
Db	628 EPCRYSYSTQKDVTGGLYPA--RATD--FQSILEENTVPMYRNFKKMEVFMSSLLIEY	682	Db 195 GTHAYMMPVPTKTFPNHYTLLATGGLYPSHSGVIGNSMVDPVEDATEFLRGREKFHNHW 254
Qy	737 ATBRNGVNVVSGPFIFDYNDGHFADPDBITHKHA-NTDVPIPTHYFVVLTSCKNKSHTPE	795	Qy 251 HQGPWMLTAMYQGLKATTFWPGSEVAINGSFSPIYMPYNGSYFPEERISTLKLWLDPK 310
Db	683 VQCHHVVTVAVGVPVDFDNGNGRDSDFLILMSGTNNKVKVIFSDIVLITCQKDSSLN	742	Db 255 GGQPLWITATKQGYRAGTFEW-----SVSPHERRLTLLQWSLUPD 296
Qy	796 NCGFWLWDYLPFIPHPRPNN-ESCP-EGKPEALWVERFTAHARVDRDVELLTGDFYQD	853	Qy 311 AERPFFTYNFEPPDSSFGAGGPVSYARVTKALOYDVAFGMLMEGLKORNLNHCVN1ILL 370
Db	743 DCYSNKTBSFVPPNSDYYNESCSRENITSVSYVRKFSLHRVTDIETVTSMSFYRN	802	Db 297 NERPSVYAYSEQDFSGHKYGPGPPEWTNPLREIDKTVGQLMDGLQKLKHRCVN1IVF 356
Qy	854 KIQPVSEELQKTYL	868	Qy 371 ADHGMDQTYCNKMEYMTDFPRINFFYMEGPAPIRAHNIPHDFFSPNSEEIVRNLSSCR 430
Db	893 VRTSSNNVAYLKYM	817	Db 357 GDHGNEVDTCRDTFLSNLYNTNVDDITLVPTGLGRIR-----PK1PNNLKCFK 403
RESULT 8			
		Q91VZ7	PRELIMINARY; PRT; 195 AA.
		ID Q91VZ7	PRELIMINARY; PRT; 195 AA.
		AC Q91VZ7;	
		DT 01-DBC-2001 (TREMBLrel. 19, Created)	DR 01-DBC-2001 (TREMBLrel. 19, Last sequence update)
		DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DR 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
		DB ENP3.	DB Similar to alkaline phosphodiesterase.
		OS Mus musculus (Mouse).	OS Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Buteleostomi; Eutherot; Mefazo; Chordata; Sciurognathi; Muridae; Murinae; Mus.
		GN ENPP2.	GN NCBI_TaxID=10090; NCBI_TaxID=10090;
		OS Mus musculus (Mouse).	OS SEQUENCE FROM N.A.
		OC Eukaryota; Metazoa.	OC TISSUE=Breast tumor; STRAINE FROM N.A.
		OC Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OC STRAINE FROM N.A.
		OX NCBI_TaxID=1.0090;	OX DR MGD; MGI:2143402; Enpp3.
		RN STRAINC57BL/6J;	RN DR GO:0016787; Phosphodiester activity; IEA.
		RN TISSUE=Hypothalamus;	RN DR GO:0009117; P-nucleotidase activity; IEA.
		RN PubMedID:22354683; Published=12466851;	RN DR InterPro; IPB002591; Phosphodiester; InterPro; IPRO01212; Somatomedin_B.
		RA The RATTOM Consortium.	RA DR Pfam; PF01033; Somatomedin_B; 2.
		RA The RIKEN Genome Exploration Research Group Phase I & II Team;	RA DR SMART; SMO0201; SO; 2.
		RT "Analysis of the mouse transcriptome based on functional annotation of full-length cDNAs."	RT DR PROSITE; PS0024; SOMATOMEDIN_B; 2.
		RL Nature 420:563-573 (2002).	RL DR SEQUENCE; 195 AA; D64F2CB37EPE4A65 CRC64;
		DR MGD; AK038940; BAC30174.1; -.	DR DR GO:00016787; Phosphodiester activity; IEA.
		DR InterPro; IPR001290; Enpp2.	DR DR GO:0009117; P-nucleotide metabolism; IEA.
		DR InterPro; IPR001212; Somatomedin_B.	DR DR InterPro; IPR001212; Somatomedin_B.

QY	1	MESTIILATEQPKKTKTQKTKYKIACTVLLALIVINSGLIGIGLGLRKLEQSGCRKKCFD	60	OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots;
Db	1	MDSRLALATEEPIKDKSLK2K2KILVLLALIVINSGLIGIGLGLRKPEQSGCRKKCFD	60	OC	Caryophyllales; Amaranthaceae; Spinacia.
QY	61	ASFRGLENCRDVACDQRGDCWDFDTCVESTRIMCNKRCGETRLEASLCSDDCL	120	ON	NCB_—TaxID=1562;
Db	61	SSHRGLEGRCDSGTGRGDCWDFDTCVSTO1WTCNLFRGCRNLEFA LCSADDCL	120	RN	SEQUENCE FROM N.A.
QY	121	QRKDCCADYKSYCQGETSWLBEENCDTAQQSQCQSPGFDLPPVTFSDMGFAEYLYWTDTL	180	RA	Sonoda M., Ide H., Sato T., Nakagawa H.; Cloning and deduced amino acid sequence of a nitrate reductase inactivator (NRI) from spinach leaves identifies a nucleotide pyrophosphatase. (SEP-1999) to the EMBL/GenBank/DBJ databases.
Db	121	QRKDCCADYKTYCQGSPWTEACASSOQPCCPQFDLPPVTFSDMGFAEYLYWTDTL	180	RT	EMBL; AB032413; BAB20681.1;
QY	181	MPININKLKTG 191	DR	GO: 0016787; F: nucleotide metabolism; IEA.	
Db	181	LPNINKLSSKG 191	DR	GO: 0009117; P: nucleotide metabolism; IEA.	
QY	Q9H515	PRELIMINARY; PRT; 152 AA.	DR	InterPro; IPR022591; Phosphodiester; 1.	
AC	Q9H515_	Created)	DR	Pfam; PF01663; Phosphodiester; 1.	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	DR	InterPro; IPR022591; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Q9H518_1	(Ectonucleotide pyrophosphatase/phosphodiesterase 3)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	ENPP3.	(Fragment).	DR	InterPro; IPR022591; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	PFAM; PF01663; Phosphodiester; 1.	
QX	Q9H515	SEQUENCE FROM N.A.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
PA	Q9H515_	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.	DR	InterPro; IPR022591; Phosphodiester; 1.	
DR	EMBL; AL157377; CA05481.1;	GO: GO:0004519; P: endonuclease activity; IEA.	DR	PFAM; PF01663; Phosphodiester; 1.	
DR	GO: GO:003676; P: nucleic acid binding; IEA.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DR	InterPro; IPR016404; Endonuclease.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	InterPro; IPR022591; Phosphodiester; 1.	
DR	Pfam; PF01223; Endonuclease.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	PFAM; PF01663; Phosphodiester; 1.	
SMART	SM00477; NUC_1.	SMART; SM00477; NUC_1.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
FT	SEQUENCE 152 AA; 17449 MW;	E22AD9E08483E932 CRC64;	DR	InterPro; IPR022591; Phosphodiester; 1.	
QY	724	MNDYFHSSYLKHTATERNGVNVYSGP1FDNNYDGHFDAPDTRKHLANTDVPPIPHYFV	783	DR	PFAM; PF01663; Phosphodiester; 1.
Db	1	MNDYFHSSYLKHTATERNGVNVYSGP1FDNNYDGHFDAPDTRKHLANTDVPPIPHYFV	60	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;
QY	784	LTSCKNKSHTPENCPGMWDLVPLPFIIPHRPNTVSCPEGKPKALWEEFPAHIAVRDVE	843	DR	InterPro; IPR022591; Phosphodiester; 1.
Db	61	LTSCKNKSHTPENCPGMWDLVPLPFIIPHRPNTVSCPEGKPKALWEEFPAHIAVRDVE	120	DR	PFAM; PF01663; Phosphodiester; 1.
QY	844	LLTGGLDFYQDKYQVPSBTLLQKTYLPFFETTI	875	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;
Db	121	LLTGGLDFYQDKYQVPSBTLLQKTYLPFFETTI	152	DR	InterPro; IPR022591; Phosphodiester; 1.
Q9FS13	PRELIMINARY;	PRT; 479 AA.	DR	PFAM; PF01663; Phosphodiester; 1.	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Nucleotide pyrophosphatase-like protein.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	SPNPLP_1.	SPNPLP_1.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Spinacia oleracea (Spinach)	Spinacia oleracea (Spinach)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Nucleotide pyrophosphatase-like protein.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	SPNPLP_1.	SPNPLP_1.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OS	Spinacia oleracea (Spinach)	Spinacia oleracea (Spinach)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
AC	Q9FS13	Created)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DR	PFAM; PF01663; Phosphodiester; 1.	
DE	Hypothetical protein DKFZp68G13218.	GO: GO:0004519; P: endonuclease activity; IEA.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
GN	DKFZp68G13218.	DKFZp68G13218.	DR	PFAM; PF01663; Phosphodiester; 1.	
OS	Homo sapiens (Human)	Homo sapiens (Human)	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
NCB_—TaxID=9606;	NCB_—TaxID=9606;	NCB_—TaxID=9606;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP94 CRC64;	
RN	Q9FS13	PRELIMINARY;	DR	SEQUENCE 479 AA; 53122 MW; 14B8C05F4FB6FP9	

Query Match 15.5%; Score 746; DB 4; Length 274;
 Best Local Similarity 54.5%; Pred. No. 5.3e-55;
 Matches 140; Conservative 37; Mismatches 78; Indels 2; Gaps 2;
 Qy 322 EEDSSGHAGGPVPSARYKALQVVDIAGMLMEGLKORNLANCVNTILLADHGMQDQTYCN 381
 3 EEDSSGHAGGPVPSARYKALQVVDIAGMLMEGLKORNLANCVNTILLADHGMQDQTYCN 381
 Db 382 KHEYMTDWPFRINFFYMEGPAPRIRAHNTPHDFSENSEEITVRNLSCREPDQHEFKPYLT 441
 Qy 63 KYTLNKLQGDYKRNIVKYGPAARLPSDVFDKYYSFNVEGJARNUSCREPNQHKPKYLR 122
 Db 442 PDPDKRKLHAYKQVNRIDKWHFIDQOWLAVRKRSNTNCGGHHGYNNEFRMEAFLAAG 500
 Db 123 HFPKRLHEFAKSDRIEPFTYDFDQMLALNSERKYGCSFFGSDNFNSMQLFVGIG 182
 Qy 501 PSFKEKTEVPEPFNIEYVNLMDLRLQIOPAPNGTHSLSNLKVPFYEPEHAAEVSKFS 560
 Db 183 PGPKHGTIADTFNIEYVNLMDLNLITPAAPNGTHSLSNLKRNPFYTPKHPREVHLV 242
 Qy 561 VCGFANPLPTESLDCCFC 577
 Db 243 QCPFTTRN-PRDNLGSC 258

RESULT 12

Q9S83 PRELIMINARY; PRT; 496 AA.

AC Q9S83; PRELIMINARY; PRT; 496 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Nucleotide pyrophosphatase-like protein (EC 3.6.1.9).

GN T16L4.190 OR AT429680

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX [1]; -TAXID=3702;

RN SEQUENCE FROM N.A.

RA Bevan K., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,

RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RA Entian K.-D., Mewes H.W., Lemcke K., Mayer K.-F.X.,

RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN SEQUENCE FROM N.A.

RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL079344; CAB45228.1;

DR EMBL; AL161575; CAB79726.1; -.

DR PIR; T09391; T09391.

DR GO; GO:0016781; F:hydrolase activity; IEA.

DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.

DR InterPro; IPR002591; Phosphodiester.

DR Pfam; PF01663; Phosphodiester; 1.

KW Hydrolase.

SQ 496 AA; 54676 MW;

8DC2B346121D732 CRC64;

DR Q42974; -

DR SEQUENCE FROM N.A.

RC STRAIN=TAINUNG 67;

RC Hsing Y.-C., Tao C.-V., Chow T., Hsieh J., Chen 2.;

RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=CV, IR44;

RC Hsing Y.-I.C., Hsu T.-F., Chen Z.-Y., Chung M.-C., Tsou C.-H.,

RA Hsieh J.-S.;

RT "Characterization of a rice early embryogenesis specific gene OSE4.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]

RN SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RC Sasaki T., Matsumoto T., Yamamoto K.;

RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC

RT clone: P0419B01.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR U25430; AAA67067.1; -.

DR AF245483; AAF65459.1; -.

DR AP003244; BAB56086.1; -.

DR PIR; T03293; T03293.

DR Gramene; Q42974; -

DR GO; GO:0016781; F:hydrolase activity; IEA.

DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.

DR GO; GO:009117; P:nucleotide metabolism; IEA.

DR InterPro; IPR02591; Phosphodiester.

DR Pfam; PF01663; Phosphodiester; 1.

KW Hydrolase; Signal.

Query Match 15.5%; Score 746; DB 4; Length 274;

Best Local Similarity 54.5%; Pred. No. 5.3e-55;

Matches 140; Conservative 37; Mismatches 78; Indels 2; Gaps 2;

Qy 322 EEDSSGHAGGPVPSARYKALQVVDIAGMLMEGLKORNLANCVNTILLADHGMQDQTYCN 381

Db 382 KHEYMTDWPFRINFFYMEGPAPRIRAHNTPHDFSENSEEITVRNLSCREPDQHEFKPYLT 441

Qy 63 KYTLNKLQGDYKRNIVKYGPAARLPSDVFDKYYSFNVEGJARNUSCREPNQHKPKYLR 122

Db 442 PDPDKRKLHAYKQVNRIDKWHFIDQOWLAVRKRSNTNCGGHHGYNNEFRMEAFLAAG 500

Db 123 HFPKRLHEFAKSDRIEPFTYDFDQMLALNSERKYGCSFFGSDNFNSMQLFVGIG 182

Qy 501 PSFKEKTEVPEPFNIEYVNLMDLRLQIOPAPNGTHSLSNLKVPFYEPEHAAEVSKFS 560

Db 183 PGPKHGTIADTFNIEYVNLMDLNLITPAAPNGTHSLSNLKRNPFYTPKHPREVHLV 242

Qy 561 VCGFANPLPTESLDCCFC 577

Db 243 QCPFTTRN-PRDNLGSC 258

RESULT 13

Q9S83 PRELIMINARY; PRT; 496 AA.

AC Q9S83; PRELIMINARY; PRT; 496 AA.

DT 042974 (TREMBLrel. 01, Created)

DT 042974 (TREMBLrel. 01, Last sequence update)

DE Nucleotide pyrophosphatase precursor (EC 3.6.1.9) (OSE4) (Nucleotide

DE pyrophosphatase homolog).

GN OSE4 OR P0419B01.2.

OS Oryza sativa (Rice).

OC Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=45100;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TAINUNG 67;

RA Hsing Y.-C., Tao C.-V., Chow T., Hsieh J., Chen 2.;

RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=CV, IR44;

RC Hsing Y.-I.C., Hsu T.-F., Chen Z.-Y., Chung M.-C., Tsou C.-H.,

RA Hsieh J.-S.;

RT "Characterization of a rice early embryogenesis specific gene OSE4.";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]

RN SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RC Sasaki T., Matsumoto T., Yamamoto K.;

RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC

RT clone: P0419B01.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR U25430; AAA67067.1; -.

DR AF245483; AAF65459.1; -.

DR AP003244; BAB56086.1; -.

DR PIR; T03293; T03293.

DR Gramene; Q42974; -

DR GO; GO:0016781; F:hydrolase activity; IEA.

DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.

DR GO; GO:009117; P:nucleotide metabolism; IEA.

DR InterPro; IPR02591; Phosphodiester.

DR Pfam; PF01663; Phosphodiester; 1.

KW Hydrolase.

Query Match 15.5%; Score 746; DB 10; Length 496;

Best Local Similarity 41.0%; Pred. No. 2e-54;

Matches 139; Conservative 71; Mismatches 141; Indels 17; Gaps 9;

Qy 157 DLPPVILFSDMGFRAEYLWDTLMPNINKLKGIGHSKY-MRAMYPTKPTFNPHYTIVTG 215

Query Match 14.8%; Score 712.5; DB 1.0; Length 457;
 Best Local Similarity 38.5%; Pred. No. 7.8e-52;
 Matches 166; Conservative 76; Mismatches 148; Index 41; Gaps 12;

Qy 148 QQSQCPCGFDLPPVILFSMDGFRAEVLYTWTILMPNINKLKTG3HSKY-MRAMYPTKTP 206
 Db 44 RSEQQPPKLNKVKVLLISCDGFRFGQFKTET-PTDILLISRGTEAKTG1IPVPTMTP 101

Qy 207 PHEYTIVTGLYPESHGIDINNNYDNLNKNESLSSKEQNNPAWWEQGPWMLTAMYQGLKA 266
 Db 102 PHEYSIATGGLYPASHGIMKNTDPYSGELFN---RNLAEPKWNLGEPLWVTAVNQGLMA 157

Qy 267 ATYFWPGGSEVAINGSF-PSIY-MPYNGSYVPEERISTLKLWDLPKAERPRFYTMYFES 3222
 Db 158 ATYFWPG2DVFH-KGSWNOPKGCKAPAVNSVPLERVTDLINYFDLPEREPDMALYFD 216

Qy 323 EPDSSGHAGGPGVSARYTAKALOVDHAFGMLKORNLNCVNILLADIGMDQTYCNK 382
 Db 2117 EPIQGHYGPDDPRVTEAVSKVDMGRINGLERKRVFSDVHILLDEGMVTCNCDK 276

Qy 383 MBEYMTDYPFRINFFYMMEGPAPRIRAHNIPHDFESFN----- SEEIVRN-- 426
 Db 277 VIYIDDLADWIKI-----PADWIDQYS---PVLAKNPRWKGKDVKNPQKNAELYRKME 327

Qy 427 -LSCKR--PDQEFKPKLTDPLKRLAYAKVNRIDKYLFDQMLAVRSKNTNGGGNH 483
 Db 328 ALSSGKVYANGEFIQVYLNELPQRLHYSDSRIPPLIGMSEGMYKONRYVQECGUTH 387

Qy 484 GYNNEFRMEAIFLAHGSFRKETEFPFENTEVYNNLMDDLRIQAPANNTHGSLNHL 543
 Db 368 GIDNMFFEMRS1FVGYGRFRRGKIVPSFENVQVNAVAEILGLRPAPNGSSLFTRSL 447

Qy 544 KYPFYEPHAE 554
 Db 448 -LPRGETSQVE 457

Search completed: July 6, 2004, 13:19:49
 Job time : 52 secs

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OM protein - protein search, using sw model

Run on: July 6, 2004, 12:47:02 ; Search time 18 Seconds

(without alignments)
2531.188 Million cell updates/sec

Title: US-10-005-480A-143

Perfect score: 4804

Sequence: 1 MESTITLATEQPKVNTLKK.QPVSEILQLKTYLPTFTETTI 875

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing First 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4804	100.0	875	1	NPP3_HUMAN	Q14638 h ectonucle
2	3982	82.9	875	1	NPP3_RAT	P97675 r ectonucle
3	2495	52.0	925	1	NPP1_HUMAN	P22413 h ectonucle
4	2414	50.7	905	1	NPP1_MOUSE	P06802 m ectonucle
5	2405	50.1	906	1	NPP1_RAT	Q924C3 r ectonucle
6	2111	43.9	862	1	NPP2_MOUSE	Q911E6 m ectonucle
7	2091.5	43.5	863	1	NPP2_HUMAN	Q13822 h ectonucle
8	2043.5	42.5	885	1	NPP1_RAT	Q84610 r ectonucle
9	2043.5	9.0	742	1	YCR5_YEAST	P25353 saccharomy
10	412.5	8.6	493	1	YBB6_YEAST	P39997 saccharomy
11	301	6.3	61	1	PPD1_BOVIN	P15396 bos taurus
12	130	2.7	476	1	TNAG_HUMAN	Q9uJW2 homo sapien
13	129	2.7	369	1	PP11_HUMAN	P21128 homo sapien
14	126	2.6	2004	1	YPT3_YERPE	Q8ZDJ2 yersinia pe
15	121	2.5	4543	1	LRP1_CHICK	P91517 gallus gallus
16	119	2.5	1378	1	WR52_ARATH	Q9fh83 arabidopsis
17	116.5	2.4	758	1	YA91_SCHEO	Q9J782 schizosacch
18	115.5	2.4	704	1	SSP1_BOOMO	P20613 bombyx mori
19	114	2.4	1105	1	STC_DROME	P40798 drosophila
20	114	2.4	4544	1	LRP1_HUMAN	Q07954 homo sapien
21	113.5	2.4	368	1	NOGL_HUMAN	Q9Y2C4 homo sapien
22	113.5	2.4	1808	1	TENA_CHICK	P10039 gallus gallus
23	113	2.4	474	1	KLFA_MOUSE	Q60793 mus musculus
24	112.5	2.3	322	1	PN11_SCHEO	Q10480 schizosacch
25	112.5	2.3	854	1	LDLR_CRIGR	P35950 cricetulus
26	112.5	2.3	2352	1	MOKC_SCHEO	Q9uJ4 schizosacch
27	112	2.3	873	1	LDLR_RAT	P25952 ratus norvegicus
28	111	2.3	329	1	NUCL YEAST	P08466 saccharomyces
29	111	2.3	662	1	FASI_SCHEM	P10675 schizosaccharomyces
30	111	2.3	1442	1	DPO3_UREPA	Q9Pqb4 ureaplasma
31	110	2.3	1700	1	BAR2_CHITE	Q03376 chironomus
32	110	2.3	1926	1	LPH_RABIT	P09849 oryctolagus cuniculus
33	109.5	2.3	871	1	SUL1_HUMAN	Q8iwu6 homo sapien

ALIGNMENTS

34	109	2.3	860	1	LDLR_HUMAN	P01130 homo sapien
35	108.5	2.3	2894	1	YD96_METJA	Q58791 methanococcus
36	107.5	2.2	470	1	KLF4_HUMAN	O43474 homo sapien
37	107.5	2.2	1169	1	C9DA_BACTP	O06014 bacillus th
38	107	2.2	887	1	ORP3_HUMAN	Q9H415 homo sapien
39	107	2.2	2156	1	RPL1_HUMAN	P56715 homo sapien
40	107	2.2	4655	1	LRP2_RAT	P98164 homo sapien
41	106.5	2.2	4660	1	LRP2_BAT	P98158 ratus norvegicus
42	106	2.2	1787	1	UVRA_CHLNU	Q9Pb60 chlamydiae
43	105	2.2	471	1	MM13_BOVIN	P07766 bovis taurus
44	104.5	2.2	1682	1	MSP1_PLAF3	P19398 plasma medium
45	103	2.1	787	1	ITB3_MOUSE	O54890 mus musculus

RESULT 1	NPP3_HUMAN	STANDARD;	PRT;	875 AA.		
	ID_NPP3_HUMAN					
	AC_O14638;					
	DT_28-FEB-2003	(Rel. 41, Created)				
	DT_28-FEB-2003	(Rel. 41, Last sequence update)				
	DT_28-FEB-2003	(Rel. 41, Last annotation update)				
	DE_Ectonucleotide pyrophosphatase/phosphodiesterase 3 (E-NPP 3)					
	DE_Phosphodiesterase I/nucleotide pyrophosphatase 3 (Phosphodiesterase					
	DE_I beta) (PD-I beta) (CD03C antigen) (Includes: Alkaline phosphodiesterase I (EC 3.1.4.11); Nucleotide pyrophosphatase (EC 3.6.1.9) (NPase))					
	DE_(EC 3.6.1.9) (NPase))					
	DB_NPP3 OR PDNP3,					
	OS_Homo sapiens (Human)					
	CC_Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;					
	RN_SEQUENCE FROM N.A.					
	RP_TISSUE=Prostate;					
	RC_MEDLINE=9800833; PubMed=9344666;					
	RA_Piao J.-H., Goding J.W., Nakamura H., Sano K.;					
	RA_Piao J.-H., Goding J.W., Nakamura H., Sano K.;					
	RA_RT_Molecular cloning and chromosomal localization of PD-I beta (PDNP3), a new member of the human phosphodiesterase I genes.;					
	RA_RT_new member of the human phosphodiesterase I genes.;					
	RA_RT_Wohldmann P., Le T.; Genomics 45:412-415 (1999).					
	RA_RT_function: Cleaves a variety of phosphodiester and phosphosulfate bonds including deoxynucleotides, nucleotide sugars, and NAD (By similarity).					
	CC_Catalytic Activity: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.					
	CC_Catalytic Activity: A dinucleotide + H(2)O = 2 mononucleotide.					
	CC_Subcellular Location: Type II membrane protein					
	CC_Somatomedin-B type domains.					
	CC_Database: NAME-PROW; NCBI-PROW 1.47-49(2000); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/575821061_g.htm".					
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	CC_DR_EMBL; AF05632; AAC51813; 1;					
	CC_DR_EMBL; AC00558; AA00519; 1;					
	CC_DR_Genew; HGNC:3358; ENPP3					
	CC_DR_MM; 602182;					
	CC_DR_MM; GO:0005887; C:integral to plasma membrane; TAS.					
	CC_DR_MM; GO:0004551; F: nucleotide diphosphatase activity; TAS.					
	CC_DR_MM; GO:0004528; F: phosphodiesterase I activity; TAS.					

CC successively from the 3'-hydroxy termini of 3'-hydroxy-terminated
 CC oligo-nucleotide.
 CC -!- CATALYTIC ACTIVITY: A dinucleotide + H(2)O = 2 mononucleotide.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- SIMILARITY: Contains 2 sonatomedin-B type domains.

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 CC or send an email to license@isb-sib.ch).

CC
 DR EMBL: Z47987; CPAA8029.1;
 DR EMBL: U78788; AAB61535.1; -;
 DR EMBL: D30649; BAA06333.1; -;
 DR PIR: A57080; A57080; -;
 DR InterPro: IPR001604; Endonuclease.
 DR InterPro: IPR002591; Phosphodiester.
 DR InterPro: IPR001212; Somaticmedin_B.
 DR Pfam: PF01223; Endonuclease; 1.
 DR Pfam: PF01663; Phosphodiester; 1;
 DR Pfam: PF01033; Somaticmedir_B; 2.
 DR SMART: SM00477; NUC; 1.
 DR SMART: SM00201; SO; 2.
 DR PROSITE; PS00524; SOMATOMEDIN_B; 2;
 KW Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;
 KW Multifunctional enzyme; Antigen; Polymorphism.
 FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 30 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT TRANSMEM 12 30 (POTENTIAL).
 FT DOMAIN 31 875 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 51 94 SONATOMEDIN-B LIKE 1.
 FT DOMAIN 95 139 SONATOMEDIN-B LIKE 2.
 FT DOMAIN 141 510 PHOSPHODIESTERASE.
 FT DOMAIN 605 875 NUCLEASE.
 FT ACT_SITE 206 206 BY SIMILARITY.
 FT SITE 79 81 CBLL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 280 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 533 533 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 702 702 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 789 789 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 124 124 K -> E.
 FT VARIANT 201 201 N -> V.
 FT VARIANT 596 597 SG -> NR.
 FT CONFLICT 111 111 A -> T (IN REF. 3);
 FT CONFLICT 273 273 P -> L (IN REF. 1);
 FT CONFLICT 475 476 SS -> VP (IN REF. 3).
 FT CONFLICT 814 814 N -> KP (IN REF. 3).
 SQ SEQUENCE 875 AA; 99071 MW; 4205PP63EE8A933FA CRC64;

Query Match 82.9% Score 3982; DB 1; Length 875;
 Best Local Similarity 81.3%; Pred. No. 1.9e-257;
 Matches 712; Conservative 77; Mismatches 85; Indels 2; Gaps 2;

1 MESTLTATEQPVKNTLKKYKIACTIVALLIVMSLGLGLGLRKLHQ-GSCKKCF 59
 1 MDSRLLAATTEPIKDSKRYKILCAVIALLIVTSLGLGLGLRKLPEEHGSCKKCF 60

60 DASFRGLNCRDQVAKDQGDCWDFDFTCVCBSTRWNCNKFRCGETRLEASLCSCDC 119

61 DSSERGLLECRDGSCTGRGDCWDFDFTCVCSTQIWCNSPRCGETRLEALCSADC 120

120 LQKEDCCADYKSYCQGETSWLENCDTAQSQCPEGFLPPVILFSDGERAEYLWTDT 179

121 LQKEDCCATYKAVCQGETPWVTRACASQEPQCPBGFQOPPVILFSDGFRAEYLWT 180

CC	QY	180 LMPNINKLKTGTHSKYMRAMYPTKTPNHYTIVTGLYPSHGIIDNNMYDVLNNQFSL 239
CC	Db	181 LLPNINKLKTGHSKMRAMYPTKTPNHYTIVTGLYPSHGIIDNNMYDVLNNQFSL 240
CC	QY	240 SSKEDQDIAWTHGQPMUHTYQGLKATATYQGLKATATYQGLKATATYQGLKATATYQGLKQFPERI 299
CC	Db	241 SSVERKSNPAWWSQCPWITAMYQGLKASYYWPGSDAVNGSPNTRNYSNVPBESRI 300
CC	QY	300 STLLKMLDLPKAASRPRFPTMYFEPDSSGHAGGPVASRVIKALQVYDHAFCMIMEGLKQR 359
CC	Db	301 ATLLQWDLPKAASRPRFPTYYEEDPSAGHRSQGPVAVKALQVYDHAFCMIMEGLKQR 360
CC	QY	360 NLANCVNILLAHQMDOTYCNKMEYMTDYPBINNFFYMEYGPAPTRAHNIPHDFFESN 419
CC	Db	361 NLANCVNILLAHGMDOTYCNKMEYMTDYPBINNFFYMEYGPAPTRAHNIPHDFFESN 419
CC	QY	420 SEEIVRNLSCRKPDQHFKPVLTDLPRKLHYAKNVRIDKVLFLVQDQWMLAVRSKSNFNG 479
CC	Db	420 SEEIVRDLSCRKSDQHFKPVLTDLPRKLHYAKNVRIDKVLFLVQDQWMLAVRSKSNFNG 479
CC	QY	480 GGNHGYNNEFRSMEATIPLAHGSPFKEKEVEEPENNIVYNLMCDLRLIQAPNNGTHGSL 539
CC	Db	480 GGTGYNNEFRSMEATIPLAHGSPFKEKEVEEPENNIVYNLMCDLRLIQAPNNGTHGSL 539
CC	QY	540 NHLLKVPYEPSEPHAEVSKPSVCGFANPLPTESEVYNNLCKDLYREYTSFGKZAMRPMWSSYVPGDTSPLPP 659
CC	Db	540 NHLLKVPYEPSEPHAEVSKPSVCGFANPLPTESEVYNNLCKDLYREYTSFGKZAMRPMWSSYVPGDTSPLPP 659
CC	QY	600 ITATKVNLPFGPRVPLQKVDHCLLYREYTSFGKZAMRPMWSSYVPGDTSPLPP 659
CC	Db	600 VSATEKTNLPFGPRVQKRNKDCILYREYTSFGKZAMRPMWSSYVPGDTSPLPP 659
CC	QY	660 TVPDOLRADYRVPPESQKCSFPLADKNTGHLGPPASNRTSDSQYDALITSNLVPMYE 719
CC	Db	660 TVPDOLRADYRVPPESQKCSFPLADKNTGHLGPPASNRTSDSQYDALITSNLVPMYE 719
CC	QY	720 EFKRWMDYFHSVLLJKHATERGYNVWSGPIDFYDGHFADPDEITHLANTDVPDIPTH 779
CC	Db	720 EFKRWMDYFHSVLLJKHATERGYNVWSGPIDFYDGHFADPDEITHLANTDVPDIPTH 779
CC	QY	780 YFVYVLTSCNKSHPENCPGWLDPFLPHTHRPNVESPECGKPEALVVEERTHTAHLRV 839
CC	Db	780 YFVYVLTSCNKSHPENCPGWLDPFLPHTHRPNVESPECGKPEALVVEERTHTAHLRV 839
CC	QY	840 RDVELLTGDFQDKVQPYSEILOLKTLPFTETTI 875
CC	Db	840 RDVELLTGDFQDKVQPYSEILOLKTLPFTETTI 875
CC	RESULT 3	SEQUENCE FROM N.A.
CC	ID NPP1_HUMAN	STANDARD; PRT; 925 AA.
CC	AC P22413; Q9NP23; C91IP6; Q9UP61; Q9Y6K3;	AC
CC	DT 01-AUG-1991 (Rel. 19, Created)	DT
CC	DT 28-FEB-2003 (Rel. 41, Last sequence update)	DT
CC	DT 28-FEB-2003 (Rel. 41, Last annotation update)	DT
CC	DE Ectonucleotide pyrophosphatase/phosphodiesterase 1 (E-NPP 1)	DE
CC	DE (Phosphodiesterase I/nucleotide pyrophosphatase 1) (Plasma-cell membrane glycoprotein in PC-1) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) (NPPase).]	DE
CC	DE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	DE
CC	OC NCBITaxonID=9606;	OC
CC	RN	RN
CC	RP	SEQUENCE FROM N.A.
CC	RX	MEDLINE=910902; PubMed=2211644;
CC	RA	Buckley M.F., Loveland K.A., McKinstry W.J., Garson O.M., Godirig J.W.;
CC	RT	"Plasma cell membrane glycoprotein PC-1. cDNA cloning of the human molecule, amino acid sequence, and chromosomal location.";
CC	RT	J. Biol. Chem. 265:1750-1751 (1990).
CC	RL	[2]
CC	RN	[2]

RP SEQUENCE FROM N.A. RX MEDLINE=92246539; PubMed=1315502; RA Nakashiba T., Kato H., Horie K., Yano T., Hori Y., Kobayashi H., Inoue T., Suzuki H., Fukui S., Tsukahara M., Kajii T., Yamashin I.; "Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase"; RT Arch. Biochem. Biophys. 295:180-187(1992). RL [3]

RP SEQUENCE FROM N.A. RX MEDLINE=99408501; PubMed=10480024; RA Bozzali M., Pizzutti A., Trischitta E.; "Genomic structure of the human PC1 gene"; RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases. RN [4]

RP SEQUENCE OF 81-925 FROM N.A. RX Peck A.; RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases. RN [5]

RP SEQUENCE OF 145-185 FROM N.A. AND VARIANT GIN-173. RX MEDLINE=95054801; PubMed=95054801; RA Pizzutti A., Frittitta L., Argiolas A., Baratta R., Goldfine I.D., Bozzali M., Ercolino T., Scarriato G., Iacoviello L., Vigneri R., Tassi V., Trischitta V.; RT "A polymorphism (K121Q) of the human glycoprotein PC-1 gene coding region is strongly associated with insulin resistance.,"; RL Diabetes 48:1881-1884(1999). RN [6]

RP CHARACTERIZATION. RX MEDLINE=95054801; PubMed=9001561; RA Belli S.I., Goding J.W.; RT "Biochemical characterization of human PC-1, an enzyme possessing alkaline phosphodiesterase I and nucleotide pyrophosphatase activities"; RT Eur. J. Biochem. 226:433-443(1994). RN [7]

RP ACTIVE SITE. RX MEDLINE=95235270; PubMed=737162; RA Mercuri P.A., Sall A., Goding J.W.; RT "Autophosphodiesterase I (alkaline phosphodiesterase I/nuclease Pyrophosphatase) and analysis of the active site"; RT Eur. J. Biochem. 228:669-676(1995). RL [8]

RP VARIANTS OPLL PRO-91 AND PHE-287, AND VARIANTS GLN-173; HIS-268 AND PRO-779. RX MEDLINE=99381541; PubMed=10453738; RA Nakamura I., Ikegawa S., Okuda S., Koshizuka Y., Kawaguchi H., Nakamura K., Koyama T., Goto S., Toguchida J., Matsushita M., Ochi T., Takaoka K., Nakamura Y.; RT "Association of the human NPPs gene with ossification of the posterior longitudinal ligament of the spine (OPLL)."; RT Hum. Genet. 104:492-497(1999). RL [9]

CC -I- FUNCTION: Has a broad specificity and cleaves a variety of substrates, including phosphodiester bonds of nucleotides and nucleotide sugars and pyrophosphate bonds of nucleotides and nucleotide sugars. -Can hydrolyze nucleoside 5'-triphosphates such as ATP, GTP, CTP, UTP and UTP to their corresponding monophosphates with release of pyrophosphate. Can hydrolyze diadenosine polyphosphates and 3',5'-cAMP to AMP. It may play a role in the regulation of pyrophosphate production, the regulation of the availability of nucleotide sugars in the endoplasmic reticulum and Golgi, and the regulation of purinergic signaling. CC -I- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides. CC -I- SUBUNIT: Homodimer; disulfide-linked. CC -I- SUBCELLULAR LOCATION: Type II membrane protein. CC -I- TISSUE SPECIFICITY: EXPRESSED IN PLASMA CELLS AND ALSO IN A NUMBER OF NON-SYMPATHETIC TISSUES, INCLUDING THE DISTAL CONVOLUTED TUBULE OF THE KIDNEY, CHONDRYCYTES, AND EPIDIDYMIS. CC -I- PTM: Autophosphorylated as part of the catalytic cycle of phosphodiesterase/pyrophosphatase activity. CC -I- PTM: N-glycosylated.

CC -I- DISEASE: Defects in ENPP1 are a cause of increased susceptibility for ossification of the posterior longitudinal ligament of the spine (OPLL), a common form of human myelopathy with a prevalence of as much as 4% in a variety of ethnic groups. CC -I- SIMILARITY: Contains 2 somatomedin-B type domains. CC -I- DATABASE: NAME=PROW; NOTE=PROW 2.32.44 (2001); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/31658143_g.htm".

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CC DR EMBL; M57736; AAF63237; 1; ALT-INIT. DR EMBL; D12485; BA02054; 1; ALT-INIT. CC DR EMBL; AF110304; AAF36094; 1; JOINED. DR EMBL; AF110280; AAF36094; 1; JOINED. DR EMBL; AF110281; AAF36094; 1; JOINED. DR EMBL; AF110283; AAF36094; 1; JOINED. DR EMBL; AF110284; AAF36094; 1; JOINED. DR EMBL; AF110285; AAF36094; 1; JOINED. DR EMBL; AF110286; AAF36094; 1; JOINED. DR EMBL; AF110287; AAF36094; 1; JOINED. DR EMBL; AF110288; AAF36094; 1; JOINED. DR EMBL; AF110289; AAF36094; 1; JOINED. DR EMBL; AF110291; AAF36094; 1; JOINED. DR EMBL; AF110292; AAF36094; 1; JOINED. DR EMBL; AF110293; AAF36094; 1; JOINED. DR EMBL; AF110294; AAF36094; 1; JOINED. DR EMBL; AF110295; AAF36094; 1; JOINED. DR EMBL; AF110296; AAF36094; 1; JOINED. DR EMBL; AF110297; AAF36094; 1; JOINED. DR EMBL; AF110298; AAF36094; 1; JOINED. DR EMBL; AF110299; AAF36094; 1; JOINED. DR EMBL; AF110300; AAF36094; 1; JOINED. DR EMBL; AF110301; AAF36094; 1; JOINED. DR EMBL; AF110302; AAF36094; 1; JOINED. DR EMBL; AF110303; AAF36094; 1; JOINED. DR EMBL; AF1242020; CAC39442; 1; JOINED. DR EMBL; AF1242021; CAC39442; 1; JOINED. DR EMBL; AF1242022; CAC39442; 1; JOINED. DR EMBL; AF1242023; CAC39442; 1; JOINED. DR EMBL; AF1242024; CAC39442; 1; JOINED. DR EMBL; AF1242025; CAC39442; 1; JOINED. DR EMBL; AF1242026; CAC39442; 1; JOINED. DR EMBL; AF1242027; CAC39442; 1; JOINED. DR EMBL; AF1242028; CAC39442; 1; JOINED. DR EMBL; AF1242029; CAC39442; 1; JOINED. DR EMBL; AF1242030; CAC39442; 1; JOINED. DR EMBL; AF1242031; CAC39442; 1; JOINED. DR EMBL; AF1242032; CAC39442; 1; JOINED. DR EMBL; AF1242033; CAC39442; 1; JOINED. DR EMBL; AF1242034; CAC39442; 1; JOINED. DR EMBL; AF1242035; CAC39442; 1; JOINED. DR EMBL; AF1242036; CAC39442; 1; JOINED. DR EMBL; AF1242037; CAC39442; 1; JOINED. DR EMBL; AF1242038; CAC39442; 1; JOINED. DR EMBL; AF1242039; CAC39442; 1; JOINED. DR EMBL; AF067177; AAD38421; 1; JOINED. DR PIR; A3916; A39216; JOINED. DR Genew; HGNC:3356; ENPP1. DR MIM; 173335; JOINED.

RT and analysis of expression."; RT PRO. Natl. Acad. Sci. U.S.A. 82:8619-8623 (1985).
 [5] RN PARTIAL SEQUENCE; RX MEDLINE:85056399; PubMed:3917281;
 Stearns P.A., van Driel I.R., Grego B., Simpson R.J., Godding J.W. "The murine plasma cell antigen PC-1: purification and partial amino acid sequence."; RT J. Immunol. 134:443-448(1985).
 [6] RN DISEASE; RX MEDLINE:9832479; PubMed:9662402;
 Okawa A., Nakamura T., Goto S., Moriya H., Nakamura Y., Ikegawa S. "Mutation in Nps in a mouse model of ossification of the posterior longitudinal ligament of the spine."; Nat. Genet. 19:271-273(1998).
 -!- FUNCTION: Has a broad specificity and cleaves a variety of substrates, including phosphodiester bonds of nucleotides and nucleotide sugars and pyrophosphate bonds of nucleotides and nucleotide sugars. Can hydrolyze nucleoside 5'-triphosphates as ATP, GTP, CTP, UTP and URP to their corresponding monophosphates with release of pyrophosphate. Can hydrolyze diadenosine polyphosphates and 3',5'-CAMP to AMP. It may play a role in the regulation of pyrophosphate production, the regulation of the availability of nucleotide sugars in the endoplasmic reticulum and Golgi, and the regulation of purinergic signaling (By similarity).
 -!- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminating oligo-nucleotides.
 -!- CC CATALYTIC ACTIVITY: A dinucleotide + H(2)O = 2 mononucleotide.
 -!- CC SUBUNIT: Homodimer; ds-sulfide-linked.
 -!- CC SUBCELLULAR LOCATION: Type II membrane protein.
 -!- CC ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 Name=2;
 CC IsoId=P06802-1; Sequence=displayed;
 Name=1;
 CC IsoId=P06802-2; Sequence=VSP 006748;
 -!- CC TISSUE SPECIFICITY: SELECTIVELY EXPRESSED ON THE SURFACE OF ANTIBODY-SECRETING CELLS.
 -!- CC PM: Autophosphorylated as part of the catalytic cycle of phosphodiesterase/pyrophosphate activity (By similarity).
 -!- CC PM: The N-terminus is blocked.
 -!- CC DISEASE: Defects in ENPP1 are the cause of the tipro walking (ttw) phenotype. Ttw mice exhibit ossification of the spinal ligaments.
 -!- CC SIMILARITY: Contains 2 somatomedin-B type domains.

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 EMBL; J02700; APA39893; 2; -.
 EMBL; M12552; APA39892; 1; -.
 MGD; MGI:97370; Enpp1.
 GO; GO:0001501; P:skeletal development; IMP.
 InterPro; IPR001604; Endonuclease.
 InterPro; IPR000591; Phosphodiester.
 InterPro; IPR001212; Somatomedin_B.
 Pfam; PF01223; Endonuclease; 1.
 Pfam; PF01663; Phosphodiester; 1.
 Pfam; PF01033; Somatomedin_B.
 PRINTS; PR0002; SOMATOMEDIN_B.
 SMART; SM00477; NUC; 1.
 SMART; SM02021; SO; 2.
 PROSITE; PS0054; SOMATOMEDIN_B; 2.
 Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;

b	b	b	b	b	b	b	b	b	b
687	DDFSNCLYQDLRIPSPVHEKCSYYKSNSKLSYGFPLPPRNLRVSHIYEALLTNSIVPM	746							
718	YEEFRKQWDYEFVSLILKHATERNGVNVSQPIFDNYDGHFDPADDEITKH--LANTDV	774							
747	YQSFQVWHLTDLQYAFERNGVNVSQPVDFDGYRDSDLEILKQNSVRQSQEI	806							
775	PIPTHYFVVLTSCKRSKHTPENCPGWLDLVSFIIPHRPTVYESCPKGKEPAWVWEERFTA	834							
807	LIPTHFFVLTSCQKQISETPPLECSA-LESSAVILPQRPDNTESCTHGKRESSWIBLLTL	865							
835	HIARYDVEILTGDFYQDKYQPVSEELQKTYLPIF	871							
866	HRARTDVEILTGASFYQDREBSVSEELLRLKTHLPIF	902							

RESULT 5					
PP1			PP2		
PP1	RAT	STANDARD	PRT;	906 AA.	
C	NPPL	Q91XQ3 ; Q92C8C ;			
C	C	Q92C8C ; Q91XQ3 ;			
T	T	28-FEB-2003 (Rel. 41, Last sequence update)			
T	T	28-FEB-2003 (Rel. 41, Last annotation update)			
T	T	Ectonucleotidase Pyrophosphatase/Phosphodiesterase 1 (B-NNP 1)			
E	E	(Phosphodiesterase 1/nucleotide Pyrophosphatase 1) (Plasma-cell membrane glycoprotein PC-1) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide Pyrophosphatase (EC 3.6.1.9) (NPPase)].			
E	E	ENPL 1.0 OR PDNP1 OR PC1 OR NPPase.			
S	S	Rattus norvegicus (Rat).			
C	C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
X	X	[1] _TaxID=10116;			
P	P	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.			
C	C	Louvain, and Wistar;			
C	C	STRAIN=Lewis; MEDLINE=22117315; PubMED=12121276;			
A	A	Banakh I., Sali A., Dubrjevic V., Grobien B., Siegers H., Goding J.W.,			
T	T	"Structural basis of allotypes of ecto-nucleotide pyrophosphatase/phosphodiesterase (plasma cell membrane glycoprotein PC-1) in the mouse and rat, and analysis of allele-specific			

Eur. J. Immunogenet. 29:307-313 (2002).
-1-
FUNCTION: Has a broad specificity and cleaves a variety of substrates, including phosphodiester bonds of nucleotides and nucleotide sugars and pyrophosphate bonds of nucleotides and nucleotide sugars. Can hydrolyze nucleoside 5' triphosphates such as ATP, GTP, CTP, TTP and UTP to their corresponding monophosphates with release of pyrophosphate. Can hydrolyze diadenosine polyphosphates and 3',5'-cAMP to AMP. It may play a role in the regulation of pyrophosphate production. It may play a role in the regulation of pyrophosphate production. The regulation of the availability of nucleotide sugars in the endoplasmic reticulum and Golgi, and the regulation of purinergic signaling (By similarity).

Isoid=Q924C3-1; Sequence=Displayed;
Name=;;
Isoid=Q924C3-2; Sequence=VSP_006749;
-|- PTM: Autophosphorylated as part of the catalytic cycle of
-|- phosphodiesterase/protophosphatase activity (By similarity).
-|- SIMILARITY: Contains 2 somatotropin-B type domains.

QY	3.03 LKWLIDLPAERPRFETYMFPEPDSSGHAGGPPSARVIALQVVDHAFGMILGKORNLL 362
Db	33.6 LEWQLQPLSPYERPHFPTLYLEBPDSSGHSHCPVSSSEVIALQKVHDHVGMMLDGLDGLD 395
QY	36.3 NCVNILLADHGMDTYCNKEMTYDYPFRINFFYMEGAPRIRAHNTPHDEFSNSEE 422
Db	39.6 KCLNLJLISDHGMEGCSCKVYVILNKYLGDVNTVYVGPAAIRLPTVEETYISFNEYA 455
QY	42.3 IVRNLSCKRPDQHFKPYLTDPDLPKRLHYAKVNRIDKVHLYFDQDN-LAYRSKSNTNCGGG 481
Db	45.6 LAKNLSCRETNQHFPPYLKHFPLKRLHFAKNDRTEBLPTFLDPOQALNPSRERYCQSGG 515
QY	48.2 NHGYNNEFRSMEAFLANGPSFKERKEFPEPFENIEVYNLMCDLRLIQAPNNNGTHGSLNH 541
Db	51.6 PHGSDNLFSNMQALFQIGYGPFAKKGAEVDSFENIEVYNLMCDLGLLIPAPNNNGHSGLNH 575
QY	54.2 LIKVPYFEBSHAESVSKPSVCGFAMPPLPTESLDCPCPHLQNSTOLEQYQMLNLTQEELT 601
Db	57.6 LIKRPKTPSPHCKEESFSLSQC---PIKVSQSDIGCTCOPDSTIVPMDFERQFQNLNTDAVE 631
QY	60.2 ATVKVNLPGRPVYLQRNVDHCLLYREVSGFGRAMPMWSSYTVPLQGDSPLPPTVY 661
Db	63.2 DYSMTIVENGRPANLQOKOHRVCLLHQHQQLTGYSLDLMPLWTSYF--LSNDQFSTDDE 689
QY	66.2 PDCLRADYRVPPSESOCSFYLADKNITHGFLYPPASNRTSDSOY-DALITSNLYPMYEE 720
Db	69.0 SNCLYQDRIPLSPMHCSSYKSTSDSYGLTPRPLNRVSRQYSEALLTSNIVPKYQS 749
QY	72.1 FRRKWDYFPHSVLLIKATERGNTVNSSPFIDNYDGHFDAPD--EITKHLANTDVIP 777
Db	75.0 FQVIVQYLHDTVLRRYAQERGNNTVNSSPFEDDYGRYDSSETLKLQNTVRSQENLIP 809
QY	77.8 THYFVLTTSCKNKSHTPENCPGMWLDLPLF1PHRPTNVCSPPGKPEALWVEERFTAHIA 837
Db	81.0 THFFIVLTLTSCKQKLSSESPKCTA-LESSAFLPHRPDNLESCTHGKQESAWELLALHRA 868
QY	83.8 RYRDVLLTGTGLDYDQKVPQSEILQLKTYLPTF 871
Db	86.9 RYTDVLLTGTGLSPYQDQESSELLRUXTHLPIF 902
RESULT 6	
NPP2_MOUSE	
AC	'09R16; 099LG9;
DT	28-Feb-2003 (Rel. 41, Created)
DT	10-Oct-2003 (Rel. 41, Last sequence update)
DE	Ectonucleotide pyrophosphatase/phosphodiesterase 2 (E-NPP 2)
DE	(Phosphodiesterase I/nucleotide pyrophosphatase 2) (Phosphodiesterase I alpha) (PD-Ialpha) [Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) (NPPase)].
GN	NPP2 OR NPPS2
OS	Mus musculus (Mouse)
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=C57BL/6;
RX	MEDLINE-2016917; PubMedID:10702660;
RA	Piao J.-H., Matsuda Y., Nakamura H., Sano K., the gene encoding phosphodiesterase I/nucleotide pyrophosphatase 2, to mouse Chromosome 15D2. ;
RA	Cytogenet. Cell Genet. 87:172-174 (1999). ;

RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Garninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W., Villalon D.K., Muzny D.M., Soederberg E.J., Iu X., Gibbs R.A., Raha J., Hellon E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green D.B., Dickson M.C., Rodriguez A.C., Grimwade J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzewinski M.J., Skalnitsa U., Smalius D.E., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RT	- - - CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.
RT	- - - CATALYTIC ACTIVITY: A dinucleotide + H ₂ O = 2 mononucleotide.
RL	- - - SUBCELLULAR LOCATION: Type II membrane protein.
CC	- - - SIMILARITY: Contains 2 somatomedin-B type domains.
CC	-----
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CC	-----
DR	EMBL; AP123542; AAD4640.1; -.
DR	EMBL; BC003264; AAH03164.1; -.
DR	MGD; MGI:1321390; Enpp2.
DR	InterPro; IPR01604; Endonuclease.
DR	InterPro; IPR02591; Phosphodiester.
DR	InterPro; IPR021212; Somatomedin_B.
DR	InterPro; IPR01223; Endonuclease_1.
DR	Pfam; PF01653; Phosphodiester_1.
DR	Pfam; PF01033; Somatomedin_B.
DR	PRINTS; PRO00022; SOMATOMEDINB.
DR	SMART; SM00477; NUC_1.
DR	SMART; SMC0201; SO_2.
DR	PROSITE; PS00524; SOMATOMEDIN_B.
KW	Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase; Multifunctional enzyme.
FT	DOMAIN 1 11
FT	TRANSMEM 12 30
FT	ACT SITE 126 209
FT	DOMAIN 31 862
FT	DOMAIN 54 97
FT	DOMAIN 98 142
FT	DOMAIN 144 501
FT	DOMAIN 597 862
FT	SITE 126 128
FT	CARBODY 53 53
FT	CARBODY 410 410
FT	CARBODY 524 524
FT	CARBODY 806 806
FT	CONFICT 517 517
FT	CONFICT 550 550
FT	CONFICT 573 573
FT	CONFICT 743 743
SEQUENCE	862 AA; 98886 MW; C43144D8A85A55 CRC64;
SQ	-----

CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Db	189 IELRSQGTHSPYMPYPPCTCFPNUYLTATGLYPSBHGIVGNSMYDPVFDATFHLSRE 248
CC	DR EMBL: L35594; AA0464785_1; -.	Qy	244 QNPAAWHRGQPMWLTANYQGKAAATYFWPGEVAINGSPSIYMPYNGVFFEBRISTL 303
CC	DR EMBL: L46720; AAB00855_1; -.	Db	249 KENHRWIGGQPIWITATKQYKACFFW-----SVVIPH-----ERRILTL 290
CC	DR EMBL: D4421; BAA08260_1; -.	Qy	304 KWDLPLKAERPRFYTMYFEPDSSSHAGGSPVSARVITALQVVDHAFGMLQQRNHN 363
CC	DR EMBL: BC034961; AAH34961_1; -.	Db	291 QMLTLPHERPSVATYSEQFDSGHKYGPFGPENTNPRLREIDKVGQMDGLKQLXLR 350
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR GO; GO:0005897; C: integral to plasma membrane; TAS.	Qy	364 CNTILILADEGNDQTCYKNEYMITYFPRINFFYMEGPAPRTR--HARNIPDFFSNS 420
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR GO; GO:0004551; F: nucleotide diphosphatase activity; TAS.	Db	351 CUNVIFGDHAGMEDVTCRTEFLSNLTNTVDITLPGTGLGRSKFSNNAKYD----P 405
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR GO; GO:000928; P: cell motility; TAS.	Qy	421 EELVRNLISCKEDQHEPKYLTPLDPLKRLHYAKSTRIDKYLFLYDQOW----LAVRSKS 474
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR GO; GO:0006796; P: phosphate metabolism; TAS.	Db	416 KAIJANDJCKCQDQHEPKYLTPLDPLKRLHYAKSTRIDKYLFLYDQOW----LAVRSKS 465
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR InterPro; IPR001604; Endonuclease.	Qy	475 NTNC-GGGNHYNNPFSMSEAFLAHGSPSKKEKTEVEPPENIETYNLMACDILRIGPDRN 533
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR InterPro; IPR001212; Phosphodiester.	Db	466 SCRCEFGDHRDNKNSMQTIVFQYQPTKVKRPPVPEIILYNNCDLIGKPNN 525
Genev; HGNC: 33:3:1; MIM: 601060; -.	PFam: PF00022; Somatomedin_B.	Qy	534 GTHGSTMTLILKDEYERSHAEVSKFESVCGFANPLPTESLDLFC- PHQONSTOLEQVQNM 592
Genev; HGNC: 33:3:1; MIM: 601060; -.	PFam: PF001223; Endonuclease_1.	Db	522 GTHGSILHLLTNTFPPTMPBENTPNTPYRIMYLQSDFLQGCTDDKBEPKNQDLEINRK 585
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane_Repeat; Signal-anchor; Hydrolase;	Qy	593 INLTQERIATATVKNLPGPRPLQKNDHCLLYKREPTYSGEKAMRNPMASSYTVPQLG 652
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Alternative splicing.	Db	586 LFTK---GSTEERHLYGPAVLY-TEYDILYHDTDFSGSEIFLPLWTSYTVXQA 640
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Alternative splicing.	Qy	653 DTSPLPLPTVPGDCLADVRVPPSESOHKCSFLADKNTIHFPLYPASNTSDQYDALITS 712
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Alternative splicing.	Db	641 EVSSVPHPLTSCKVPRVSPFSQNCNLAYKNDQMSGFLFPYLSPEAKYDAFVLT 700
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR PRINTS; PRO00022; SOMATOMEDIN_B.	Qy	713 NLVPVMEBFKRWMDYHPSVLLKHATERVNVSGPFLPDYNYDGHFPAPDDEITKHLANT 772
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR SMART; SM00201; SO; 2.	Db	701 NMVPMYPAFKRWMDYHPSVLLKHATERVNVSGPFLPDYDGLHLTDKTKQYVEGS 760
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR PS00324; SOMATOMEDIN_B; 2.	Qy	773 DVP1PHTYFVVLTSCKNSKSHTPENCPGWLDPFLPTIIPRPTNYESCPGSKPEALWVERF 832
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;	Db	761 6IPVPHYKYYLTSITSLQFTPADKCDGPUSVSSETLHRPDNECSNSSEDESKWVEELM 820
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;	Qy	833 TAHIARYRDVELLGLDIFYQDKVQEVSEIOLKTYLPFETTI 875
Genev; HGNC: 33:3:1; MIM: 601060; -.	DR Glycoprotein; Transmembrane; Repeat; Signal-anchor; Hydrolase;	Db	821 KQHTARVDRDISHLTSIDFRKTSRSYPEILTKTYLHRYSEI 863
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT TRANSMEM 11 30	RESULT 8	FT/FTid=VSP_006750;
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT TRANSMEM 12 30	NPBP2_RAT	STANDARD; PRT; 885 AA.
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 1 11	AC	Q64610; ID NPBP2_RAT
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 12 30	DT	28-FEB-2003 (Rel. 41, Created)
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 31 863	DT	28-FEB-2003 (Rel. 41, Last annotation update)
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 55 98	DE	Ectonucleotide Pyrophosphatase/phosphodiesterase 2 (E-NPP 2)
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 99 143	DE	(phosphodiesterase 1/nucleotide Pyrophosphatase 2) (Phosphodiesterase I
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 145 502	DE	(EC 3.1.4.1. (PD-1alpha) [Includes: Alkaline Phosphodiesterase I
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT DOMAIN 598 863	DE	GN ENPP2 CR NPBP2.
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT ACT SITE 210 210	OS	Rattus norvegicus (Rat).
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CARBOHYD 127 129	OS	SEQUENCE FROM N.A.
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CARBOHYD 54 54	RC	STRAIN-Sprague-Dawley; TISSUE=Brain;
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CARBOHYD 99 411	RC	MEDLINE=950605; PubMed=7961762;
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CARBOHYD 525 525	RA	Narita M., Goji J., Nakamura H., Sano K.;
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CARBOHYD 807 807	RT	"Molecular cloning, expression, and localization of a brain-specific
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT VARSPLIC 324 324	RT	phosphodiesterase I/nucleotide pyrophosphatase (PD-1alpha) from rat
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 23 23	RT	brain";
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 73 73	RT	J. Biol. Chem. 269:28235-28242 (1994).
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 100 100	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 291 291	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 349 349	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 629 629	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 644 644	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 703 703	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	FT CONFLICT 769 769	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	SQ SEQUENCE: 863 AA; 99003 MW;	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	9 SCQISLFFAVGVNCLGFTAHRIKAEGWEEGPPVTLSPWNISGSGCKGRCPLOE 68	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	64 RGLENCRVACKDRGDCWDFDTCVYESIWCMNKRFCRTEASLSCSDICLQK 123	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	69 AGPPDCRCMNCJCSYTSCHDFDECLKTAARGWCTKDRCEVREENAHFCSECLARG 128	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	124 DCCADYKSYCQGETSWLBNCDTAQQSCPEGFDLPPVILFSMDGFRAYLYTWDLMN 183	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	129 DCCTNYQVVKCGSHWDDCEKIFAKAECPAGEVRPLIFSVDFGRASMYKCKSKWPN 188	RT	
Genev; HGNC: 33:3:1; MIM: 601060; -.	184 INLKTKGHSKYMARMYPTKTPFPNHTIVTGLYPBSSHGILDNNMYDVNLNKNSLSSKE 243	RT	

Query Match Score 2091.5%; DB 1; Length 863;
Best Local Similarity 43.1%; Prod. No. 5.3e-142; Mismatches 267; Gaps 10;

Matches 381; Conservative 176; Mismatches 267; Gaps 10;

Sequence: 24 ACIVLLAVIMVSLGGLGKRLKLEK-----QGSCRKICFDASF 63

- CATALYTIC ACTIVITY: Hydrolytically removes 5'-nucleotides successively from the 3'-hydroxy termini of 3'-hydroxy-terminated oligo-nucleotides.
- CATALYTIC ACTIVITY: A dinucleotide + H₂O = 2 mononucleotide.
- SUBCELLULAR LOCATION: Type II membrane protein.
- TISSUE SPECIFICITY: Abundantly expressed in cerebrum and cerebellum. Localized in secretory epithelial cells in the brain and the eye including choroid plexus epithelial cells, ciliary epithelial cells, iris pigment epithelial cells, and retinal pigment cells.
- SIMILARITY: Contains 2 somatomedin-B type domains.

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D28560;	BAA05910.1;	-.
ATIR; A55453;	A55453.	Endonuclease;
InterPro; IPR001604;		Endonuclease;
InterPro; IPR000591;		Phosphodiester;
InterPro; IPR001212;		Somatomedin_B.
PF01223; PF01656;		Endonuclease; 1.
PF01656; PF01033;		Phosphodiester; 1.
PF01033; SOMATOMEDINB.		Somatomedin_B; 2.
PRINTS; PRO0022;		SOMATOMEDINB.
SMART; SM00477;		NUC; 1.
SMART; SM00201;		SO; 2.
PROSITE; PS00524;		SOMATOMEDIN_B; 2.
PROSITE; PS00524; SOMATOMEDINB;		Transmembrane; Recept;
		Signal-anchor; Hydrolase;
		CYTOSOLIC (POTENTIAL).
CONANIN	11	SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
CONANIN	10	
CONANIN	12	
CONANIN	13	

Query Match	42.5%	Score	2043.5	DB 1,	Length	885;
Best Local Similarity	41.7%	Prod. No.	1.5e-138;			
Matches	380;	Conservative	178;	Mismatches	275;	Indels
Qy	14	KENTLKKYKIAIVLALLIVMSLGLGGLGLRKIEK				-QGSC 54
Db	3	RQGCLGSQVISLFTFAI	---	SYNCLGFTASRKKRAEWDEGPPFTLSDSPWNTNSGSC	58	
Qy	55	RKKCFDASFRGLENCRCYDACKDRGDCMWFEDTQVESTRIMMNKFRGCTREASLCS	114			
Db	59	KGRFCFELQEVGPPDORCDNLCKSYSSCCSDDEFLCKTVGWECKDRSCEVRNEACH	118			
Qy	115	CSDDFLCKEDCCADYKSYSCGEGTLEENCDTAQSQCPGFSDL--PPVILFSMGFMFRA	172			
Db	119	CPEFLSRSQEDCCTINYQVVKCGESEHIV--DDAARNQSSECLQVPPPLIFSVGFRAS	174			
Qy	173	YLYTWDLMPNINKLTKTGTHSKYKMRAMYPTKTFPHNHTLVGTPESHGLIDNNYDYN	232			

Qy	233	LNCFSLSKESKEONPAWHGQPMWLTAMYQQKRAITYKALQVQDHA.FGML	352	FWGESEAVINGSFS.LININGS 292
Db	235	FDASFHILGREGKEHNHRWGGQQLWITATQGYTRAGIEFW-	-----	-----SVS 276
Qy	293	VPPPERISTLXWIDLPKAERPRFTYMFEEPDSSGHAGGPVSARYTKALQVQDHA.FGML	352	-----
Db	277	IPHRRLITLQMSLSPNERSVAYSEQDFSGKYGKPGPENTNPLERIDKYGQI	336	-----
Qy	353	MEGLKQNLHNCYNTILLADHGMDQTCNKMEYMTDFPRINFFYMEGAPRIRAHNP 412	-----	
Db	337	MDGKIKOLRHLRCVNFYGDHGNBVDTCDRTFSLNTLNVIDTILVPGTUGRIRAKSIN	396	-----
Qy	413	HDFPSFNSHEVANLSTCKPDKQHCKPFLTPDLPKLYAKNVRIDKYLFDQW-----	467	
Db	397	NS--KYDPTTIANLTCKPDKDQHCKPVMKQHLPKLYANNEERIEDHLLVDRRHVARK	454	
Qy	468	-LAYRSKSNTNC--GGNNGYNNERSMSMEAIFLAHHGPSKEXTKEPPENIEVYNNLMDLL	525	
Db	455	PLDVKKPKBGGKCP?FGDGDGDKWVNSMOTYFUGYGPPTKRYKVPKPPPNELYNMCDLL	514	
Qy	526	RIOAPPNNGTHGSISNLHLKVPFPSSHAEVSKSVCFCANPLPTESLDCFC- PHLNQST	584	
Db	515	GLKAPPNNGTHGSISNLHLRNTNTPMDEVSRSRNP?GIMYLOSEFDIGCTCDKVEPKN	574	
Qy	585	QLEQYQNMNL-----TQEETATVRY---NLPFGRPVRLQKNDVHC	623	
Db	575	KLEENKRLTKGSTEAEETGKFRRSHENKRNLLNGSVEPKRHLLYGRPAVLY-TSYD	633	
Qy	624	LLYHREYVSSGFCKAMRMPKNSSYVTPQLGDTSPLPPTVDPDVRVPPSESQKCSFYL	683	
Db	634	LLYHDTDFESCYSEFLPPYLSSPEAKYDFTLNVNMPVYAPCRWVAFQRLVVKYASERNGV	753	
Qy	684	ADKONTHGFLLYPPASNRTSDQYDALTISNLVPMYEEFRKMDYHPSVLLKHATERGV	743	
Db	694	NDKQNSYGFELPPYLSSPEAKYDFTLNVNMPVYAPCRWVAFQRLVVKYASERNGV	753	
Qy	744	NVVSQPIFDNYDGHEDAPPBITHGLANTDVPITHFVVLTSKKNKSHTPENCPGMLDV	803	
Db	754	NVISQPIFDNYDGLRDTDEBKQYVEGSSIPVYHTISITSLDFQPADICDGPSLV	813	
Qy	804	LPPFIIPIRPTNVESCPEKGKPEALWYEEERTFAHIAVRDVELLTGDFYDVKVQVSEELQ	862	
Db	814	SSPFLPFRPDNDESNSSEDESKEWVEELKMHTRDIEHTLGDFYRKTSSYSELT	873	
Qy	864	LKTYLJPTFETTI	875	
Db	874	LKTYLHTYESEI	885	
RESULT 9				
YCR6 YEAST				
ID	YCR6 YEAST	STANDARD	PRT;	742 AA.
AC	P25359; QBN1L9;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hypothetical protein YCR226C.			
GN	YCR26C OR YCR246.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.			
OX	NCBI TaxID=932;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAINS-S288C;			
RX	MEDLINE:92244356; PubMed:1574125;			
RA	Oliver S.G.; van der Hart Q.J.M.; Agostoni-Carbone M.L.; Aigle M.';			
RA	Alberghina L.; Alexander D.; Antoine G.; Anwar R.; Ballesta J.P.G.,			
RA	Bergantino B.; Berben G.; Bittau N.; Bolle P.-A.,			
RA	Bolten P.; Brown R.; Buhler J.M.';			
RA	Bozzi-Fukuhara M.; Brown J.P.; Crouzet R.; Daquinan-Fornier B.,			
RA	De Haan M.; Defoor E.; Delgado M.D.; Demolder J.; Doira C.,			
RA	Dubois E.,			

RA	Fairhead C.A., Faye G., Feldmann H., Fiers W.,	266	AATYFMPGPSEY-----AINGSEPPSYMPYNGSVPFEBRISTULKWLDDL
RA	Francignes-Gaillard M.-C., Franco L., Frontali L., Fukuhara H.,	285	AATHKMPGSDNYTKNEEKLQPEHKNP1FARERTPFYFDEFNAKEPLSOKLSK1EY7DM
RA	Fuller L.J., Gent M.E., Gigot D., Gilliquet V., Glassdoeff N.,		
RA	Goffeau A., Grenson M., Grisantti C.J., Grivell L.A., Haasemann M.,		
RA	Hatat D., Hegmann J.H., Herbert C.J., Hilger F., Hohmann S.,		
RA	Hollen D., C.P., Huse K., Ilorra P., Indge K.J., Isono K., Jackman P.,	309	PKA-BEPRFVITYMPEPDSSGHAGPVSAR-----VIKALQVYDHAFCM1MEGLKORN1
RA	Jagg C., Jacquet M., James C.M., Janniaux J.-C., Jia Y., Jimenez A.,		
RA	Kleinmans U., Kreissl P., Lafanchi G., Lewis C., van der Linden C.G.,		
RA	Luccinelli G., Lutzenkirchen C., Maat C., Mannhaupt G., Manzano M.E.,		
RA	Marzegani E., Matheiu A., Maurer C.T.C., McConnel D., McKee R.A.,		
RA	Messenguy P., Mewiss H.W., Mollemans F., Montagne M.A., Navas L.,		
RA	Newton C.S., Olson M.V., Paliard C., Panzeri L., Pearson B.M.,		
RA	Pereira J., Philippin P., Pierard A., Plantz R.J., Plevani P.,		
RA	Poersch B., Pohl F.M., Purnelle B., Ramezani Rad M., Rasmussen S.W.,		
RA	Raynal M., Remacha M., Richerich P., Roberts A.B., Rodriguez F.,		
RA	Sanz E., Schaff-Serstenschaeger I., Scherens B., Schweitzer B.,		
RA	Shu Y., Skala J., Slonimski P.P., Sor P., Soustelle C.,		
RA	Spiegelberg R., Staeteva L.I., Steensma H.Y., Steiner S., Thierry A.,		
RA	Thireos G., Triano L.N., Urestarazu L.A., Valle G., Vetter I.,		
RA	van Vliet-Reedijk J.C., Volicckaert G., Vreken P., Warmington J.R.,		
RA	von Wettstein D., Wichtstone B.L., Wilson C., Wurst H., Xu G.,		
RA	Zimmermann F.K., Sgourou J.G.,		
RT	"The complete DNA sequence of yeast chromosome III.;"		
RL	Nature 357:38-46(1992).		
RL	[2]		
RP	SEQUENCE OF 244-742 FROM N.A.		
RP	MEDLINE:92245758; PubMed=1574926;		
RA	Bolle P.-A., Gilliquet V., Berben G., Dumont J., Hilger F.,		
RT	"The complete sequence of K3B, a 7.9 kb fragment between PK1 and		
RT	CRY1 on chromosome III, reveals the presence of seven open reading		
PT	frames;"		
PT	yeast 8:205-213 (1992).		
RN	[3]		
RP	REVISIONS.		
RA	Valles G., Volckaerts G.,		
RL	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.		
CC	-!- SIMILARITY: TO YEAST YEL01CC.		
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distinct segments of the developing human nephron.";

RL Connect. Tissue Res. 37:53-60(1998).

CC -!- FUNCTION: Mediates adhesion of proximal tubule epithelial cells via integrins alpha3-beta1 and alpha5-beta3.

CC -!- SUBCELLULAR LOCATION: Basement membranes.

CC -!- ALTERNATIVE PRODUCTS: Basement membranes.

CC Event=Alternative splicing; Named isoforms=2;

CC Name=TIN1L;

CC IsoId=09UJTW2-1; Sequence=Displayed;

CC Note=Major isoform;

CC Name=TIN2;

CC IsoId=09UJTW2-2; Sequence=VSP_050567, VSP_050568;

CC -!- TISSUE SPECIFICITY: Expressed in the kidney cortex, small intestine and cornea.

CC -!- DEVELOPMENTAL STAGE: Initially observed in the Bowman's capsule during early glomerular capillary loop formation in the kidney. In more developmentally mature glomeruli, following transition from early to mid-capillary loop stage, expression is higher in the proximal tubular basement membrane than in the distal basement membrane and Bowman's capsule.

CC -!- DISEASE: Antibodies against TINAG are found in sera of patients with tubulointerstitial nephritis, a rare autoimmune disorder that causes acute and chronic renal injury.

CC -!- SIMILARITY: Belongs to peptidase family C1.

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CC -!- EMBL: AB02277; BAA8949_1; -;

CC EMBL: AF195116; AAFA08331_1; -;

CC EMBL: AF195117; AAFA08932_1; -;

CC PIR: JCT189; JCT189.

CC HSSP: P07688; 10DQ.

CC MEROPS: C01_973; -;

CC Genew; HGNC:14599; TINAG.

DR MIM: 607649; -;

DR GO: GO:0005604; C:basement membrane; IDA.

DR GO: GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO: GO:0070155; P:cell adhesion molecule activity; IDA.

DR InterPro: IPR006668; Peptidase Cl.

DR InterPro: IPR009041; PMP_inhibitor.

DR InterPro: IPR001212; Somatomedin_B.

DR Pfam: PF00112; Peptidase Cl; 1.

DR ProDom: ProDom158; Peptidase_Cl; 1.

DR SMART; SM00645; Peptidase_Cl; 1.

DR SMART; SM030201; SO; 1.

DR KW Cell adhesion; Extracellular matrix; Basement membrane; Glycoprotein; Alternative splicing.

FT VARSPLIC 209 300 Missing (In isoform TIN2).

FT FTID=VSP_050567.

FT CONFLICT 7 8 F8 -> IL (IN REF. 1).

FT CONFLICT 175 175 N -> I (IN REF. 2; AAF08932).

FT CONFLICT 199 199 P -> L (IN REF. 1).

FT CONFLICT 333 333 D -> H (IN REF. 1).

FT CONFLICT 381 381 R -> H (IN REF. 1).

FT CONFLICT 421 421 L -> R (IN REF. 2; AAF08932).

FT CONFLICT 437 437 P -> S (IN REF. 1).

FT CONFLICT 463 463 V -> I (IN REF. 1).

FT SEQUENCE 476 AA; 54646 MW; 32DE88E3083C3077 CRC64;

Query Match 2.7%; Score 130; DB 1; Length 476;

Best Local Similarity 21.4%; Pred. No. 0.083; Gaps 13;

Matches 56; Conservative 29; Mismatches 69; Indels 108; Gaps 13;

Qy 75 CKDRGDDCCMFEDTCVESTRIMCNKFRCGETRLEASLCSDDC-LQKDDCCADYKSVC 133

Db 57 CRNFG-CCEDRDDGV--TEFYAA-

Qy 134 QGETSW-----LEEND-----TAQQSQCPEGFDL--PPV- 162

Db 103 REEKWPPIHTQPWVPEGCFKDQIYEVEGSVTKENNSCTSGQWQKCSOHVCLVRPELIE 162

Qy 163 -----LFSMDGPRAEYLYTNDLMPNINKLKTGTHSKYMRAMYPT 203

Db 163 QVNKGDDGTAQNYSQFWGNTLEDGFK---FRGLTLPSPMLLS---MNEWTAISLPA 213

Qy 204 KTFPNHHTIVTGLYPE-SHGIID---KNNYDYNLNNKES 238

Db 214 TTDLPEFFVASYKWPWTHGPQKRNCAASWAFSTASVADRIAQSKGRTANLSPQNL 273

Qy 239 LSSKEQN-----NPAAWH 251

Db 274 ISCCAKNRHGCGNSGSIDRAWY 295

RESULT 13

PP11_HUMAN STANDARD; PRT; 369 AA.

ID PP11_HUMAN AC P21128; DT 01-FEB-1991 (Ref. 17, Created) DT 01-FEB-1991 (Ref. 17, Last sequence update)

DB Placental protein 11 precursor (EC 3.4.21.-) DE Homo sapiens (Human).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Embio: Eutheria; Primates; Catarrhini; Hominidae; Homo. OC NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-29.

RC TISSUE:Placenta; RX MEDLINE=90274860; PubMed=2350428;

RA Grundmann U.; Reimisch J.; Siebold B.; Bohn H.; Amann E.; RT "Cloning and expression of a cDNA encoding human placental protein 11, a putative serine protease with diagnostic significance as a tumor marker.", RT DNA Cell Biol. 9:243-250 (1990). [2]

RN RP SOMATOMEDIN-B TYPE DOMAIN. RX MEDLINE=91248172; PubMed=1710108;

RA Jenne D.; RT "Homology of placental protein 11 and pea seed albumin 2 with vitronectin." RBL Bichem. Biophys. Res. Commun. 176:1000-1006(1991).

CC -!- FUNCTION: Probable serine protease.

CC -!- MISCELLANEOUS: PLACENTAL PROTEIN 11 IS A PLACENTAL-SPECIFIC PROTEIN BUT IS ALSO ASSOCIATED WITH VARIOUS MALIGNANT NEOPLASMS.

CC -!- SIMILARITY: Contains 1 somatomedin-B type domain.

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CC EMBL; M32402; PAA3464_1; DR EMBL; M36109; AAA34465_1; DR PIR; A34614; A34614.

CC MIM: 606720; -; DR GO; GO:0005615; C:extracellular space; TAS.

CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.

CC GO; GO:0008236; F:fering-type peptide activity; TAS.

InterPro: IPR001212; Somatomedin_B.
 Pfam: PF0103; Somatomedin_B; 1.
 SMART: SM00201; SO; 1.
 PROSITE: PS00524; SOMATOMEDIN_B; 1.
 DR: KW Hydrolase; Serine protease; Signal; Polymorphism.
 SIGNAL 1 18 PLACENTAL PROTEIN 11.
 PT CHAIN 19 369 SOMATOMEDIN_B-LIKE.
 DOMAIN 45 89 E -> Q (in dbSNP:6504).
 PT VARIANT 31 31 /FTid:VAR_014733.
 PT VARIANT 31 31 E -> V (in dbSNP:6505).
 PT /FTid:VAR_14794.
 SQ SEQUENCE 369 AA: 42121 MW: F5935AE12D7E924C CRC64;
 Query Match 2.7%; Score 129; DB 1; Length 369;
 Best Local Similarity 19.3%; Pred. No. 0.069;
 Matches 71; Conservative 48; Mismatches 104; Indels 140; Gaps 17;
 Qy 53 SCRKKCFDASFRGLENCRDIYACKDRDCCVDFEDRCVESTRIMCNKFRCGETPLEASL 112
 Db 48 SCGRCYEA-FDKHHQHCHCNARQEFQNCNCCRDPELSCSDHE- 87
 Qy 113 CSCDDDC1QKDCDACYKSVCOGETSMLE-----ENC---DIAQQ-SQCPEGFDLDP 159
 Db 88 VSHSSDAITKEEQTISISKIYADTKNAQKEDIVANSQNCTISPSERTRNQVDRCPKP--- 143
 160 PTIIFSMDFRAEYLWTDLMPNINKTGTGHSKYMRAVYPTKTFPHHYTIVTGLYPE 219
 Db 144 ---LFT---YVNEKLFRSPRTYAFINL-----ANNQRAT--- 173
 Qy 220 SHGLIDNNMYDVNLNKQFSLSSKEQNPNPAWQHGPMLTAMYQGKAAATYFWPGSEVAIN 279
 Db 174 -HG------EHSAQELAEQPAFL---REMTKAVNKELY--- 203
 280 GSFBPSIYHNGSYVPFERIRSTLKLWLDLPAERPRPTYTMFEEDPSGHAGGPYSARI 339
 Qy 204 -SFLHHQHRYGSEQFVDDLNKM---WFL-----YSRGNEEGDSSG--- 241
 340 KALQVVDHAEGMNEGLKORNHLNCVNILLADHGMDCOTYCNRMETMDYPRINPFMY 399
 Db 242 -----FEHVFSGEVYKKGTVTFHWR-----YLEEKEGLVDDYSHI---Y 280
 Qy 400 EGP 402
 Db 281 DGP 283

RESULT 14
 YP73_YERDE STANDARD; PRT; 2004 AA.
 ID YP73_YERDE
 AC Q8ZJ2; (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-DEC-2003 (Rel. 42, Last annotation update)
 DE Hypothetical UPF0192 protein YP02573/Y1143 precursor.
 GN YP0573 OR Y1143.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersiniae.
 RN [1] NCBI_TaxID=632;

SEQUENCE FROM N.A.
 STRAIN:CO-92 / Biovar Orientalis;
 MEDLINE=2147013; PubMed=1158360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 Prentice M.B., Sebastián M., James K.D., Churcher C., Mungall K.L.,
 Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarzaga A.M.,
 Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 Feltwell T., Feltwell T., Hamlin N., Hollord S., Jagesh K., Karlyshev A.V.,
 Leather S., Moulle S., Oyston P.C.F., Quail M.A., Rutherford K.,
 Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague";
 RL Nature 413:523-527(2001).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN:KIMS / Biovar Medievalis;
 RC MEDLINE=22137863; PubMed=1214230;
 RX Deng W., Burland V., Plumbett G., III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindner L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 CC -|- SIMILARITY: Belongs to the UPF0192 family.
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 DR A474152; CAC91375; 1;
 DR EMBL; AED13717; AAM84721; 1;
 DR PIR; AC0314; AC0314;
 DR HYPOTHETICAL PROTEIN; Signal; Complete proteome.
 DR PCTENTIAL.
 DR SIGNAL 1 27 2004 HYPOTHETICAL PROTEIN YP02573.
 DR PT CHAIN 1 28 2004 AA; EA9F8A1E7452672C CRC64;
 DR SQ SEQUENCE 2004 AA; 224130 MW; EA9F8A1E7452672C CRC64;
 DR DR 2.6%; Score 126; DB 1; Length 2004;
 DR Best Local Similarity 19.7%; Pred. No. 1.1;
 DR Matches 131; Conservative 89; Mismatches 258; Indels 186; Gaps 31;
 DR Query Match 2.6%; Score 126; DB 1; Length 2004;
 DR Best Local Similarity 19.7%; Pred. No. 1.1;
 DR Matches 131; Conservative 89; Mismatches 258; Indels 186; Gaps 31;
 DR Query 236 NFSLSKSEQNPNPAWQHGPMLTAMYQGKAAATYFWPGSEVAINGFP-SIYMPYNGSVP 294
 DR DR 283 NFSVTFDEKLNRATHSQP---IMMDKG-----GSVHLNSNKCNVNSAYA 324
 DR PT SIGNAL 1 28 2004 AA; EA9F8A1E7452672C CRC64;
 DR SQ SEQUENCE 2004 AA; 224130 MW; EA9F8A1E7452672C CRC64;
 DR DR 295 FEERISTLKKWLDLPAERPRFTYMFEEPDSSGHAGGPVSARV 350
 DR DR 325 ATPTQANQKWKSV-----PNLYSH-----AVNSINATLVE-----DNNGERAL 365
 DR DR 351 -MIEGLKQRNLHCVNILLADHGMDCOTYCNRMETMDYPRINPFYF-----
 DR DR 366 RIAISDAVKDKEIKAIVAKANLPPQNFQAKESAKTS-----TDFYPMDIDDNLILQQSTPL 423
 DR DR 392 -RIN-----FYYMFGPAPPIRAHNIPHDFFSNSEETIVRNLSCRKPDPDQHKPYL 440
 DR DR 424 ALTRIAEOPYOPISFKFDPASPTKLLIVNNSS-TSGVYKM-----PEKIQIVR 475
 DR DR 441 TPDLPKRLHYAKNTRIDKVLFVDQWLAVRSKSNNTNCGGNNHGYNNFPRSMEAFLFLAHG 500
 DR DR 476 VPDYKTLRFLRNSQGSL--LSMQGDRQ-ISAARNNT-----GMKLDIKRVPSPQLQH 525
 DR DR 501 PSFKETEVFENIVNIMCDLRIQPAFNNGTGSINH-----
 DR DR 526 VSFKSEYYSAHNRISDEYTFHQYQTAALNDPGEINYQGVNLDSRYANNPSARRGV 585
 DR DR 542 -LKVPFYEP-----SHAPE-----VSKFVCGFANPLTESLFCCPHLQNST 584
 DR DR 586 FULLISAWDPEKRDNQHQSESDYDQEWNGDSRFVITDGLITKQSQD-----RSRDV 640
 DR DR 585 QLEQVNQMNLTQEITATVYKVLPPGRPRVLOKNDHCLLYHREYVSGFGKAMRPMWS 644
 DR DR 641 FVQSTHSGLPAADAKYVAQNGVV-----LISQTDKGVHFPALDAF-KNERPVP- 692
 DR DR 645 SVTPQLGDTSPSLPPPTV-----DCIRADV-RVPPSESKCSFYL-ADKNITHGLYPP 696
 DR DR 693 MFLVKEKGDSVPLPTTRAYDRNLDLFSRFDGEETPSDPRTLSSYIFSDRVS-----
 DR DR 697 ASNTRSDSQYDALITSNL-----VPMYBFRKWDYFHSVLLKHATERGNVVS- 747
 DR DR 745 -YRPGDRFNGLIGITRTANWATLDGYLRAIRDPTDLNSTLPI-TLDSSGNELSY 800

Qy 748 ----GPIFDYN-YDGHFFDAPDEITKHLANTDVF----PTHYFVVLTSCKNRSHTPBNC 797
 Db 801 TTGENSPPTGWWVTVLYGKONNETSMILGHTTVKKEPFDRLKVQL---QLTPER 854

Qy 798 PGWL 801
 Db 855 QGKV 858

RESULT 15
 LRP1_CHICK STANDARD; PRT; 4543 AA.

AC P98157;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Low-density lipoprotein receptor-related protein 1 precursor (LRP)
 DB (Alpha-2-macroglobulin receptor) (A2mR).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC NCBI_TaxID=9031;
 RN 1.
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=White Leghorn; TISSUE=Liver, and Ovary;
 MEDLINE=9410321; PubMed=7506255;
 RX RA Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.;
 RT "The somatic cell-specific low density lipoprotein receptor-related
 protein of the chicken. Close kinship to mammalian low density
 lipoprotein receptor gene members";
 RT J. Biol. Chem. 269:212-219 (1994).
 CC -1- FUNCTION: Involved in the plasma clearance of chylomicron remnants
 and activated alpha 2-macroglobulin, as well as the local
 metabolism of complexes between plaminogen activators and their
 endogenous inhibitors. Binds vitellogenin, calcium and alpha 2-
 macroglobulin.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC - Event=Alternative splicing; Named isoforms=2;
 CC - Name=1;
 CC - Name=2;
 CC - ISOID=P98157-1; Sequence=Displayed;

CC - ISOID=P98157-2; Sequence=VSP_004312;

CC - TISSUE_SPECIFICITY: Somatic.

CC - PTM: Cleaved into a 85 kDa membrane-spanning subunit (LRP-85) and
 a 515 kDa large extracellular domain (LRP-515) that remains non-
 covalently associated.

CC - SIMILARITY: Contains 22 EGF-like domains.

CC - SIMILARITY: Contains 31 LDL-receptor class A domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license to license@ibb-sib.ch).

CC DR EMBL_X74904; CNA52870.1; -.

CC DR PIR; AS3102; AS3102.

CC DR PDB; 1LPX; 29-DEC-99.

CC DR InterPro; IPR000152; Asx_hydroxyl_S.

CC DR InterPro; IPR01881; EGF_Ca.

CC DR InterPro; IPR006209; EGF_Like.

CC DR InterPro; IPR02172; LDL_receptor_A.

CC DR InterPro; IPR00033; Ldl_receptor_rep.

CC DR Pfam; PF00008; EGF_14.

CC DR Pfam; PF00057; Ldl_recept_a; 31.

CC DR Pfam; PF00058; Ldl_recept_b; 33.

CC DR PRINTS; PR0026; LLRECEPTOR.

CC DR SMART; SM00192; Ldha; 31.

CC DR SMART; SM00135; LY; 34.

CC DR PROSITE; PS00010; ASX_HYDROXYL; 3.

CC DR PROSITE; PS00022; EGF_1; 5.

CC DR PROSITE; PS01186; EGF_2; 7.

CC DR PROSITE; PS50026; EGF_3; 8.

CC DR PROSITE; PS01187; EGF_Ca; 2.

CC DR PROSITE; PS01209; LDLRA_1; 27.

CC DR PROSITE; PS50068; LDLRA_2; 31.

CC KW Receptor; Transmembrane; Repeat; Endocytosis; Glycoprotein; Signal;
 KW Calcium-binding; EGF-like domain; Coated pits; Alternative splicing;

DR KW 3D-structure; 1 21
 FT SIGNAL 1 21
 FT CHAIN 22 4543
 DR KW PROTEIN 1.
 DR KW LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED
 PROTEIN 1.
 DR KW EXTRACELLULAR (POTENTIAL).
 DR KW POTENTIAL.
 DR KW CYTOPLASMIC (POTENTIAL).
 DR KW LDL-RECEPTOR CLASS A 1.
 DR KW LDL-RECEPTOR CLASS A 2.
 DR KW EGF-LIKE 1.
 DR KW EGF-LIKE 2; CALCIUM-BINDING (POTENTIAL).
 DR KW EGF-LIKE 3.
 DR KW EGF-LIKE 4.
 DR KW LDL-RECEPTOR CLASS A 3.
 DR KW LDL-RECEPTOR CLASS A 4.
 DR KW LDL-RECEPTOR CLASS A 5.
 DR KW LDL-RECEPTOR CLASS A 6.
 DR KW LDL-RECEPTOR CLASS A 7.
 DR KW LDL-RECEPTOR CLASS A 8.
 DR KW LDL-RECEPTOR CLASS A 9.
 DR KW LDL-RECEPTOR CLASS A 10.
 DR FT DOMAIN 4444 4543
 DR FT DOMAIN 4420 4443
 DR FT DOMAIN 4444 4543
 DR FT DOMAIN 27 68
 DR FT DOMAIN 72 112
 DR FT DOMAIN 113 151
 DR FT DOMAIN 152 191
 DR FT DOMAIN 476 522
 DR FT DOMAIN 801 841
 DR FT DOMAIN 850 890
 DR FT DOMAIN 891 931
 DR FT DOMAIN 932 971
 DR FT DOMAIN 972 1011
 DR FT DOMAIN 1011 1051
 DR FT DOMAIN 1058 1097
 DR FT DOMAIN 1100 1140
 DR FT DOMAIN 1141 1180
 DR FT DOMAIN 1181 1220
 DR FT DOMAIN 1221 1260
 DR FT DOMAIN 1534 1577
 DR FT DOMAIN 1842 1883
 DR FT DOMAIN 2151 2191
 DR FT DOMAIN 2472 2512
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 DR FT DOMAIN 4195 4231
 DR FT DOMAIN 4237 4267
 DR FT DOMAIN 4303 4330
 DR FT DOMAIN 4339 4374
 DR FT DOMAIN 4372 4409
 DR SITE 3942

ENDOCYTOSIS SIGNAL (POTENTIAL)			
4501	4506	Db	1.086 CMDSSDE--RNKEGVTHVCDPNVKFGKDSARCISAWCVDGSDCDEDNSDBENCSLVC 1143
DISULFID	29	Qy	88 ----TCVESTRIW--- -MCN- KFRCGETRLEASTCSCSDPCLQQKKDCCADYKSYCGE 136
DISULFID	36	Db	1.144 KPPSHTCANNSTICLPPBKLCGSDDGDGSDGECLC---DOCSLNNGCSHNTCAVAGE 1200
DISULFID	49	Qy	1.37 -----TSWLBENC-----DTAQOSQ-----CPBGFDL----- 158
DISULFID	74	Db	1201 GIVCSCPGLGMELGADDNKTQCOISYCAKHLKCSOKCEQDKYNYTCSCYBGMWLPDGECSR 1260
DISULFID	81	Qy	159 -----PPVLFs-----MDGFRAEYLYTWDLMPNINKLKTGHSKYMRAAMYPTKTF 206
DISULFID	94	Db	1261 SLDPFKFIIISNREIRRIDLHRGDIY---SVLPGIRNRTIALDFLHN-QSSUYWT--- 1312
DISULFID	117	Qy	207 PNHYTIVTGLYPSHGIIIDNNNNYDVNLINKNFSLSKE --QNNPAWHEGQPM-WLTAMYQ 262
DISULFID	122	Db	1313 -----DVVEDKTYRKCLLENGALTSFEVVIQSLATPGLAVDMI---- 1352
DISULFID	137	Qy	263 GLKAATYFWPGS---EVA-INGSFPSIYMPNGSYPEERIST-----LLKMLD---- 307
DISULFID	150	Db	1353 --AGNTYWWESNLQDEVAKLDGTMTTLLA-GDEBRPRTALDPRYGILTWTDWIDAS 1407
DISULFID	156	Qy	308 LPKAERPRF---YTMYFEEPDSSGHAGGPVSARVIKAQLOVUDHAFGMLMEGIKORNILH 362
DISULFID	166	Db	1408 LPNEAASMSGASRRTIHK---TGSGWP-----NGTVTDYLEKR--- 1445
DISULFID	175	Qy	363 NCVNILLIADHGMDQTYCNCNMEYMTDYPFRINPPMYYEGPAPTRAHN-IPHDFFSFNSE 421
DISULFID	175	Db	1446 ---ILWIDARSDAIY-----SALYDGIGHIEVLRGHEYLSHPF----- 1480
DISULFID	190	Qy	422 EIVRNLSCKRKPQDFHFKPLTPDLPKRLHYAKNVRIDKYL----- 1486
DISULFID	825	Db	1481 -----AVTLY----- 1481
DISULFID	827	Qy	482 NHGYNNEPRSMEAI---FLAHGPSFKEKTEVBPENTEVYNLMCDLIRIOPAPNGTHG 537
DISULFID	852	Db	1487 GEYWWDRTNTIAKANGWTGHNTVVTQVNTOPFD-LOVYHPSRQPLAPNPCEANGRKG 1545
DISULFID	859	Qy	538 SLNHLKVPFYEPSSHAEEVSKFSVCGFANPLPTESDLDFCPCHL---QNSTOLEVNQNM 592
DISULFID	871	Db	1546 PCSHLCL-NY-----NRTLSCACPHIMLDKDNTTCYEFKKFL 1582
DISULFID	893	Qy	593 LNLHQEBTATVKNLPF 610
DISULFID	900	Db	1584 LYARQMEIRG-VDIDNPY 1600
DISULFID	912	Search completed: July 6, 2004, 13:18:47 Job time : 21 secs	
DISULFID	912		
DISULFID	934		
DISULFID	941		
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DISULFID	2572		
DISULFID	2585		

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OM protein - protein search, using sw model

Run on: July 6, 2004, 12:45:12 ; Search time 64 Seconds

(without alignments)
 3862.954 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTMLTATEQPVKTKLKK.QPVSEIILQLKTYLPPFTETTI 875

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : A_Geneseq_29Ua04:*

- 1: GeneseqP1986:*
- 2: GeneseqP1995:*
- 3: GeneseqP2006:*
- 4: GeneseqP2001:*
- 5: GeneseqP2005:*
- 6: GeneseqP2004as:*
- 7: GeneseqP2004bs:*
- 8: GeneseqP2008:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4804	100.0	875	7	AD56099	Ad56099 Human Pro
2	4804	100.0	875	7	AD56103	Ad56103 Human Pro
3	4804	100.0	875	7	AD55891	Ad55891 Human 161
4	4804	100.0	875	7	AD55904	Ad55904 Human 161
5	4804	100.0	875	7	AD55969	Ad55969 Human 161
6	4804	100.0	875	7	AD55899	Ad55899 Human 161
7	4804	100.0	875	7	AD55983	Ad55983 Human 161
8	4804	100.0	875	7	AD55982	Ad55982 Human 161
9	4804	100.0	875	7	AD55909	Ad55909 Human 161
10	4804	100.0	875	7	AD55984	Ad55984 Human 161
11	4804	100.0	875	7	AD55991	Ad55991 Human 161
12	4804	99.9	875	7	AD55910	Ad55910 Human 161
13	4801	99.9	875	7	AD55905	Ad55905 Human 161
14	4801	99.9	875	7	AD55913	Ad55913 Human 161
15	4798	99.9	875	7	AD55897	Ad55897 Human 161
16	4798	99.9	875	7	AD55907	Ad55907 Human 161
17	4797	99.9	875	7	AD55911	Ad55911 Human 161
18	4797	99.9	875	7	AD55910	Ad55910 Human 161
19	4796	99.8	875	7	AD55901	Ad55901 Human 161
20	4795	99.8	875	6	ABG74664	ABG74664 Human
21	4743	98.7	885	4	ABG10289	ABG10289 Novel hum
22	4642	96.6	841	7	AD65989	AD65989 Human 161
23	4634	96.6	841	7	AD65903	AD65903 Human 161
24	4634	96.5	841	7	AD65990	AD65990 Human 161
25	4634	96.5	841	7	AD65988	AD65988 Human 161

ALIGNMENTS

RESULT 1
 AD56099 standard; protein; 875 AA.

ID AD56099
 XX AC AD56099;
 XX DT 29-JAN-2004 (first entry)
 XX DE Human Protein AAC51813, SEQ ID NO 1940.

XX Human; pain; neuronal tissue; gene therapy;
 XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
 XX spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WO2003016475-A2.

XX WO2003016475-A2.

XX PD 27-FBB-2003.

XX PP 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0343382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.

XX PA WOOLF C, D'urso D, Betort K, Costigan M;
 PI XX WPI; 2003-268312/26.
 DR GENBANK; AAC51813.

XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
 XX PS Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derived from a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent CC that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal.

subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at http://wipo.int/pub/published_pct_sequences.

Sequence 875 AA;

Query Match Score 4804; DB 7; Length 875;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEQPKTKNTLKYKIACTIVLLALIVMSIGLGLGLKRLKEQGSCRKKCID 60
Db 1 MBETLTLATEQPKTKNTLKYKIACTIVLLALIVMSIGLGLGLKRLKEQGSCRKCFD 60
Qy 61 ASFRGLENCRCDYACKDRGDCWDFDFTCVSTRIMCNKRCGETRLESLCSCSDDCL 120
Db 61 ASFRGLENCRCDYACKDRGDCWDFDFTCVSTRIMCNKRCGETRLESLCSCSDDCL 120
Qy 121 QKDDCCADYKSVCQGETSWLBEENCDAQSQCPEGFDLPPVTLFSMDGFRAEYLTTWDTL 180
Db 121 QKDDCCADYKSVCQGETSWLBEENCDAQSQCPEGFDLPPVTLFSMDGFRAEYLTTWDTL 180
Qy 181 MPNTINKLKTGTHSKYRNAMPTKTFPNHHTIVTGLYPESHGQTIDNNMMYVNLNKNFSL 240
Db 181 MPNTINKLKTGTHSKYRNAMPTKTFPNHHTIVTGLYPESHGQTIDNNMMYVNLNKNFSL 240
Qy 241 SKEQNNPAWWHSGPMLNTATYQGLKAATYFWPGSEVAINNSFPSTYMPYNGSYFEEFTS 300
Db 241 SKEQNNPAWWHSGPMLNTATYQGLKAATYFWPGSEVAINNSFPSTYMPYNGSYFEEFTS 300
Qy 301 TLIKWLDLPAKRPREFTYMFEEPDSSGHAGGPVSARVIALQVYDTHAFGMLMGLKRN 360
Db 301 TLIKWLDLPAKRPREFTYMFEEPDSSGHAGGPVSARVIALQVYDTHAFGMLMGLKRN 360
Qy 361 LHNCVNNTILLADHGMDTYCNKMEIMTDYPRINFYPMYEGPAPRIRAINIPHDFFSNS 420
Db 361 LHNCVNNTILLADHGMDTYCNKMEIMTDYPRINFYPMYEGPAPRIRAINIPHDFFSNS 420
Qy 421 EETVNRNLSCKRPDQHFKPYLTPDLPKRLHAKNVRIDKVLFDQWMLAVRSNTNCG 480
Db 421 EETVNRNLSCKRPDQHFKPYLTPDLPKRLHAKNVRIDKVLFDQWMLAVRSNTNCG 480
Qy 481 GNGHYNNEFRSMEIAFLAHHGFSKKEKTEVEPFENIEVNNMCDLIRIOPAPNNGTHGSIN 540
Db 481 GNGHYNNEFRSMEIAFLAHHGFSKKEKTEVEPFENIEVNNMCDLIRIOPAPNNGTHGSIN 540
Qy 541 HLLKVFYEPVSHAEEVSKFYSQCGFANPLPESLDCFCPHQNSQLEQVNQMLNLTQEBI 600
Db 541 HLLKVFYEPVSHAEEVSKFYSQCGFANPLPESLDCFCPHQNSQLEQVNQMLNLTQEBI 600
Qy 601 TATVKYNLPEGRPRVPLQKNVNDHCLLYHRETVSGFQKAMPMSSYYTPOLGDTSPLPPT 660
Db 601 TATVKYNLPEGRPRVPLQKNVNDHCLLYHRETVSGFQKAMPMSSYYTPOLGDTSPLPPT 660
Qy 661 VPDLCLRADYRVPPSESQKCCSYFLADKNITGFLYPPASRRTSDSQYDALITSNLVPMYEE 720
Db 661 VPDLCLRADYRVPPSESQKCCSYFLADKNITGFLYPPASRRTSDSQYDALITSNLVPMYEE 720

Qy 721 FRKWDYFHSVLLIKHATERNGVNVSGPFDYNYDGHFDADEBITHGLANDDVPITHY 780
Db 721 FRKWDYFHSVLLIKHATERNGVNVSGPFDYNYDGHFDADEBITHGLANDDVPITHY 780
Qy 781 FVVLTSCKNSHTPBNCPWLDLPLFIPHRPTNVESEPGKPEALVTEERTAH1FVR 840
Db 781 FVVLTSCKNSHTPBNCPWLDLPLFIPHRPTNVESEPGKPEALVTEERTAH1FVR 840
Qy 841 DVELITGLDFYQDKVQPSBILQKTYLPTFETI 875
Db 841 DVELITGLDFYQDKVQPSBILQKTYLPTFETI 875
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein AAC51813, SEQ ID NO 1944.
XX XX Human; Pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-031217P.
PR 01-NOV-2001; 2001US-0346322P.
PR 26-NOV-2001; 2001US-0333347P.
XX PA (GBHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX PA (FARB) BAYER AG.
XX PI Woolf, C, D'urso, D, Befort, K, Cossigan, M;
XX WP1, 2003-268312/26.
DR GENBANK; AAC51813.
XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
XX Claim 1; Page, 1017PP; English.
PS
XX CC The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp://wipo.int/pub/published_pct sequences.

RESULT 3
ADE65891 standard; protein; 875 AA.
ID ADE65891
YY

xx	SQ	Sequence 875 AA;
xx	Query Match	100.0%; Score 4804; DB 7; Length 875;
xx	Best Local Similarity	100.0%; Pred. No. 0;
xx	Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MESTLTLATEOPVKNTLKKYKIACTVLLALLVIMSIGLGLGKIRKLEKQGSCRKCFD 60
Db	1	MESTLTLATEOPVKNTLKKYKIACTVLLALLVIMSIGLGLGKIRKLEKQGSCRKCFD 60
Qy	61	ASFRGLENCRCDVACKDRGDCCWDFFDTCYBSTRIMCNKFRGCTERLEASLCSDDCL 120
Db	61	ASFRGLENCRCDVACKDRGDCCWDFFDTCYBSTRIMCNKFRGCTERLEASLCSDDCL 120
Qy	121	QKEDCCADYKSVCGETSWLBNCDTAQQSQCPEGFDLPPVILFSMDGFRAYLYTWDTL 180
Db	121	QKEDCCADYKSVCGETSWLBNCDTAQQSQCPEGFDLPPVILFSMDGFRAYLYTWDTL 180
Qy	181	MPNINLKTKTCIHSKMRAMYPTKTPNHTITVGTYPESHGIDINNMYDYNLNQNSFLS 240
Db	181	MPNINLKTKTCIHSKMRAMYPTKTPNHTITVGTYPESHGIDINNMYDYNLNQNSFLS 240
Qy	241	SKEQNPAWHEGQPMVLTAMYQGLKATYFPGSEVATNGSPSPIMPYNGSVPFFERIS 300
Db	241	SKEQNPAWHEGQPMVLTAMYQGLKATYFPGSEVATNGSPSPIMPYNGSVPFFERIS 300
Qy	301	TLKWDLPLKAERPRFTYMFPEPDSSGHAGGPVSARVIALQVWDAFGMLMEGIKQRN 360
Db	301	TLKWDLPLKAERPRFTYMFPEPDSSGHAGGPVSARVIALQVWDAFGMLMEGIKQRN 360
Qy	361	LHNCVNTILLADHGGMOTYCNKMEYDYPKINPFTYMEGAPRAHNTPHDFSFNS 420
Db	361	LHNCVNTILLADHGGMOTYCNKMEYDYPKINPFTYMEGAPRAHNTPHDFSFNS 420
Qy	421	BEIVRNLSCKREDQHKPVLTDPLPKRLHYAKNVRDVKVHLYDQOQLAVRSKSNTNCGG 480
Db	421	BEIVRNLSCKREDQHKPVLTDPLPKRLHYAKNVRDVKVHLYDQOQLAVRSKSNTNCGG 480
Qy	481	GNHGTNNNEFRSMEAIFLAHGSPSKETEVPEPENIETYNLMCDLRIQAPANGTGSILN 540
Db	481	GNHGTNNNEFRSMEAIFLAHGSPSKETEVPEPENIETYNLMCDLRIQAPANGTGSILN 540
Qy	541	HLLKVPPYEPSSAEESKFSVGAFPLPTSLDCPHLONSTQLEQVNOMLNQEEI 600
Db	541	HLLKVPPYEPSSAEESKFSVGAFPLPTSLDCPHLONSTQLEQVNOMLNQEEI 600
Qy	601	TATVKTNLPGCRPRVILQKNDHCLLYTREYSGFKAMRMPMWSSTVQJGDTSLPLPT 660
Db	601	TATVKTNLPGCRPRVILQKNDHCLLYTREYSGFKAMRMPMWSSTVQJGDTSLPLPT 660
Qy	661	VPDCLRADVRVPPSEOKCSFYLADKNITHGELYPASNRTSDSOYDALITSNLVPMYEE 720
Db	661	VPDCLRADVRVPPSEOKCSFYLADKNITHGELYPASNRTSDSOYDALITSNLVPMYEE 720
Qy	721	FRKMDWYHFSVLLKIKATERGVNVUSGPIPDYNDHEDADPTEITKHLANDPPIHY 780
Db	721	FRKMDWYHFSVLLKIKATERGVNVUSGPIPDYNDHEDADPTEITKHLANDPPIHY 780
Qy	781	FVVLTSCKNSKHTPENCPGMWDLPLPIPHRTNVSCPEGKPEALWVEERTAHARVR 840
Db	781	FVVLTSCKNSKHTPENCPGMWDLPLPIPHRTNVSCPEGKPEALWVEERTAHARVR 840
Qy	841	DVELLTGGLDFYDQKQPVSEIQLQKTYLPTFETTI 875
Db	841	DVELLTGGLDFYDQKQPVSEIQLQKTYLPTFETTI 875

Db	241. SKEONNPWQHGPWNKLTAMYQGLKAATYFWPGEVAINGSPSPSIYMPYNGSPVPEERIS 300	XX	A composition for diagnosing, preventing and treating cancer (e.g. prostate, renal or uterine cancer) comprises 161P2F10B polymucleotides and polypeptides.
Qy	301. TLLKWLDFKAERPRFTMYFEEPDSSCHAGGPVSARVITALQVYDHAFCMILMEGLKQRN 360	PT	
Db	301. TLLKWLDFKAERPRFTMYFEEPDSSCHAGGPVSARVITALQVYDHAFCMILMEGLKQRN 360	PT	
Qy	361. LANCVNITLILADIGMDCTYCNKBEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS 420	XX	This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancer. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 1 protein of the invention.
Db	361. LANCVNITLILADIGMDCTYCNKBEYMTDFPRINFFMVEGAPTRAHNIPHDFFSNS 420	XX	
Qy	421. EETIRNLSSRKPDGHFKYLTDPKRLHYAKNRIDKXHLEFDQWMLARSKSNTNCGG 480	CC	
Db	421. EETIRNLSSRKPDGHFKYLTDPKRLHYAKNRIDKXHLEFDQWMLARSKSNTNCGG 480	CC	
Qy	481. GNHGYNNFRSMEAIFLAHGPSKERTKEVEPPENIEVNLMCDLRLIQPAPNGTHGS.LN 540	CC	
Db	481. GNHGYNNFRSMEAIFLAHGPSKERTKEVEPPENIEVNLMCDLRLIQPAPNGTHGS.LN 540	CC	
Qy	541. HLLKVPF7EPSHAAEVSKFSVCGFANPLTESLDCFCPHLONSTLEQVNOMLNITQEEI 600	CC	
Db	541. HLLKVPF7EPSHAAEVSKFSVCGFANPLTESLDCFCPHLONSTLEQVNOMLNITQEEI 600	CC	
Qy	601. TATVKVNITLIFGRGPVLOQVDDHLLYHBYVSGCFKAMMENWSSVTPVQGDTSPLPP 660	CC	
Db	601. TATVKVNITLIFGRGPVLOQVDDHLLYHBYVSGCFKAMMENWSSVTPVQGDTSPLPP 660	CC	
Qy	661. VPDCLRADYRVPDSEQSQXCSFVLADKNITHGSLYPPASNRFSQDSDQYDALITSNLVPMYE 720	CC	
Db	661. VPDCLRADYRVPDSEQSQXCSFVLADKNITHGSLYPPASNRFSQDSDQYDALITSNLVPMYE 720	CC	
Qy	721. FROWDYPHSVLLIKHATERNGVNWVSGPFDYDGHFDAPDEITKHLANTDVP1PTHY 780	CC	
Db	721. FROWDYPHSVLLIKHATERNGVNWVSGPFDYDGHFDAPDEITKHLANTDVP1PTHY 780	CC	
Qy	781. FVVLTSCKNKSHTPENCQWLDLPLF1PHRPTNVESCPCKPEALWVEPERFTAHARYR 840	CC	
Db	781. FVVLTSCKNKSHTPENCQWLDLPLF1PHRPTNVESCPCKPEALWVEPERFTAHARYR 840	CC	
Qy	841. DVEELTGIDFYQDKVQPVSEI1QLKTYLPTFETTI 875	CC	
Db	841. DVEELTGIDFYQDKVQPVSEI1QLKTYLPTFETTI 875	CC	
RESULT 4			
ID	AD65904		
ID	AD65904 standard; protein: 875 AA.		
XX			
AC	AD65904		
XX			
DT	29-JAN-2004 (First entry)		
XX			
DE	Human 161P2F10B protein variant 1 #2.		
XX			
161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.			
XX			
OS	Homo sapiens.		
XX			
PN	W02003040340-A2.		
XX			
PD	15-MAY-2003.		
XX			
07-NOV-2002; 2002WO-US036002.			
XX			
PR	07-NOV-2001; 2001US-00005480.		
PR	31-JAN-2002; 2002US-00062109.		
XX			
PA	(AGEN-) AGENSYS INC.		
PA			
PA	07-NOV-2002; 2002WO-US036002.		
XX			
XX			
Jakobovits, A., Raitano AB, Paris M, Hubert RS, Ge W, Morrison KM;			
PI	Morrison RK, Challita-Eid PM;		
XX			
DR	WPI: 2003-441560/41.		
DR	N-PSDB; ADE65891.		
721. FROWDYPHSVLLIKHATERNGVNWVSGPFDYDGHFDAPDEITKHLANTDVP1PTHY 780			

Db	721	FRKWDYFISVLLJKHATERGNTVVNSPIFDYNDGFDADEITGHLLANTDVPITHY	780	Qy	121	QKDCDCADYKSVCOGETSMLEENCITAQQSQCPGFDLPPVILFSDGFRAEYLTYWDTL	180
Qy	781	FVVLTSCKNSKSHPPENCPGWLDPFILPPRPTNVESSPEGKPEALVVEERTAHARVR	840	Db	121	QKDCDCADYKSVCOGETSMLEENCITAQQSQCPGFDLPPVILFSDGFRAEYLTYWDTL	180
Db	781	FVVLTSCKNSKSHPPENCPGWLDPFILPPRPTNVESSPEGKPEALVVEERTAHARVR	840	Qy	181	MPNINKLKTGIGHSYKRAMYPTKFPNEYTTIVGLYPSHGLIDNNMYDYNLNNKNSLS	240
Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875	Db	181	MPNINKLKTGIGHSYKRAMYPTKFPNEYTTIVGLYPSHGLIDNNMYDYNLNNKNSLS	240
Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875	Qy	241	SKEQQNPANTHGQPMWLTAMYQGLKATAYFWPGSEVAINGSFPSIYMPNGSVPFEEIRIS	300
Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875	Db	241	SKEQQNPANTHGQPMWLTAMYQGLKATAYFWPGSEVAINGSFPSIYMPNGSVPFEEIRIS	300
RESULT 5				Qy	301	TLLKNDLPLKAERPFTYMFEEPPSSGHAGGPYSARVKALQVWDHATGMLMEGLKQRN	360
ID ADR65969	standard; protein; 875 AA.			Qy	301	TLLKNDLPLKAERPFTYMFEEPPSSGHAGGPYSARVKALQVWDHATGMLMEGLKQRN	360
ID ADR65969	standard; protein; 875 AA.			Db	301	TLLKNDLPLKAERPFTYMFEEPPSSGHAGGPYSARVKALQVWDHATGMLMEGLKQRN	360
XX				Qy	361	LHNCVNILLADHGMDOTYCNKRMEMYMTDFPRINFFYMEGPARIRAHNTIHDPEFSNS	420
AC				Db	361	LHNCVNILLADHGMDOTYCNKRMEMYMTDFPRINFFYMEGPARIRAHNTIHDPEFSNS	420
DT	29-JAN-2004	(first entry)		Qy	421	EEIVRNLSCKRPDOHFKPYLTDPDKRHYACVYR1DKYTHFLFDQWILAVRSKSNTNCGG	480
XX				Db	421	EEIVRNLSCKRPDOHFKPYLTDPDKRHYACVYR1DKYTHFLFDQWILAVRSKSNTNCGG	480
XX	Human	161P2F10B protein variant 1 #4.		Qy	481	GNHGYNNEFMSMEAFLAHCPSFKEKTEVEPFENIEEVVNLMCDLRLIQPAPNNGTHGSLN	540
XX	161P2F10B; cancer; cyostatic; gene therapy; vaccine; human.			Db	481	GNHGYNNEFMSMEAFLAHCPSFKEKTEVEPFENIEEVVNLMCDLRLIQPAPNNGTHGSLN	540
XX	Homo sapiens.			Qy	541	HLLKPYEYERSHAEVSKSVESSVCGANPLPTESELDCPHLQLNSTOLEQVNOMNLTQEBI	600
OS				Db	541	HLLKPYEYERSHAEVSKSVESSVCGANPLPTESELDCPHLQLNSTOLEQVNOMNLTQEBI	600
PN	WO2003040340-A2.			Qy	601	TATVKVNLPGRPRVLTQKNDHCLLYREHREVSQGGRKAMPMKSSYTPVQLGDTSPPLPT	660
XX				Db	601	TATVKVNLPGRPRVLTQKNDHCLLYREHREVSQGGRKAMPMKSSYTPVQLGDTSPPLPT	660
PD	15-MAY-2003.			Qy	661	VPDCIYRADYRVPSSSQKCSPSYLAQDNTHGFLYRPPSNTQLEQVNOMNLTQEBI	720
XX				Db	661	VPDCIYRADYRVPSSSQKCSPSYLAQDNTHGFLYRPPSNTQLEQVNOMNLTQEBI	720
PP	07-NOV-2002; 2002WO-US036002.			Qy	721	FRKMDYFPHSYLLKTHATERGNGNVVSGPFLDYNQDGHFDADPDTKHANTDYPPIPHY	780
XX				Db	721	FRKMDYFHSVLLKTHATERGNGNVVSGPFLDYNQDGHFDADPDTKHANTDYPPIPHY	780
PR	07-NOV-2001; 2001US-00005480.			Qy	781	FVVLTSCKNSKSHTPNCPGWLDFLPLFPHRPTNVESCPBGKPKALWYBERFTAHARVR	840
PR	31-JAN-2002; 2002US-00062109.			Db	781	FVVLTSCKNSKSHTPNCPGWLDFLPLFPHRPTNVESCPBGKPKALWYBERFTAHARVR	840
XX				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
PA	Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;			Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
PI	Morrison RK, Challita-Eid PM;			Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
XX				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
DR	WPI; 2003-441560/41.			Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
XX				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
PT	A composition for diagnosing, preventing and treating cancer (e.g. prostate, renal or uterine cancer) comprises 161P2F10B polynucleotides and polypeptides.			Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
PT	Example 65; SEQ ID NO 81; 135pp; English.			Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
PS				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
XX	This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 1 protein of the invention.			Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
XX	Sequence 875 AA;			Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Qy	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875
CC				Db	841	DVELLTGFLDFYQDKVQPVSEILQKTYLPTFETTI	875

PR 07-NOV-2001; 2001US-00005480.	Qy 601 TATVKVNLPEGRPRVQKNDHCLLYREYVSGFGKXMRMPMWSSTYVPOLGDTSPPIPPPT 660
PR 31-JAN-2002; 2002US-00062109.	Db 601 TATVKVNLPEGRPRVQKNDHCLLYREYVSGFGKXMRMPMWSSTYVPOLGDTSPPIPPPT 660
XX (AGEN-) AGENSYS INC.	
XX	
PI Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KJM;	Qy 661 VPCDILRAVYRVPSESEQCSFVLAQKITHGLYPPASNRTSDQYDALITSNLVMEYEE 720
PI Morrison RK, Challita-Eid PM;	Db 661 VPCDILRAVYRVPSESEQCSFVLAQKITHGLYPPASNRTSDQYDALITSNLVMEYEE 720
DR WPI; 2003 441560/41.	Qy 721 FROWDYPHSVLLKIHATERGNTVSGPIFYDNYDCHFDARDEIKHLANTDVP1PHTY 780
XX N-PSDB; ADE6598.	Db 721 FROWDYPHSVLLKIHATERGNTVSGPIFYDNYDCHFDARDEIKHLANTDVP1PHTY 780
PT A composition for diagnosing, preventing and treating cancer (e.g. prostatic, renal or uterine cancer) comprises 161P2F10B polymucleotides and polypeptides.	Qy 781 FVVLTSCKNKSHTPENCPCGWLDPFLIPHRPNTVSCPEGKPEALWEEERTAHARVR 840
PT XX PS Claim 1; SEQ ID NO 11; 135pp; English.	Db 781 FVVLTSCKNKSHTPENCPCGWLDPFLIPHRPNTVSCPEGKPEALWEEERTAHARVR 840
XX	
CC This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 5 protein of the invention.	Qy 841 DVELLTGFLDFYQKVKQPVSEIQLKTYLPTFETTI 875
CC XX	Db 841 DVELLTGFLDFYQKVKQPVSEIQLKTYLPTFETTI 875
CC	
RESULT 7	
CC ADE65983 standard; protein: 875 AA.	Qy 841 DVELLTGFLDFYQKVKQPVSEIQLKTYLPTFETTI 875
CC ID ADE65983	Db 841 DVELLTGFLDFYQKVKQPVSEIQLKTYLPTFETTI 875
CC AC ADE65983;	
XX DT 29-JAN-2004 (first entry)	
XX DE Human 161P2F10B protein variant 1 #5.	
XX ID ADE65983	
XX XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.	
XX XX Homo sapiens.	
XX XX WO2003010340-A2.	
XX XX 15-MAY-2003.	
XX XX 07-NOV-2002; 2002WO-US036002.	
XX XX 07-NOV-2001; 2001US-00005480.	
XX XX 31-JAN-2002; 2002US-00062109.	
XX XX PA (AGEN-) AGENSYS INC.	
XX XX PI Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KJM;	
XX XX PI Morrison RK, Challita-Eid PM;	
XX XX DR WPI; 2003-441560/41.	
Qy 1 MESTPLTATEQPKNTLKKYKACIVLALLIVMSIGLGLGLKLEKQGCSRKKCFD 60	
Db 1 MESTPLTATEQPKNTLKKYKACIVLALLIVMSIGLGLGLKLEKQGCSRKKCFD 60	
Qy 61 ASFRLGLENCRDVAQKDRGDCMDFEDTCVESTRIMCNKFRGCGTRLEASLCSDDCL 120	
Db 61 ASFRLGLENCRDVAQKDRGDCMDFEDTCVESTRIMCNKFRGCGTRLEASLCSDDCL 120	
Qy 121 QKDCCADYKSVSQGETSWLEENCDTAQSQPEGPDLPPVILFSMDGFAEYLWTDTL 180	
Db 121 QKDCCADYKSVSQGETSWLEENCDTAQSQPEGPDLPPVILFSMDGFAEYLWTDTL 180	
Qy 181 MNPINKLKGTHSKYMEAMYPTKTFPNHHTIVTGLYPESHGIDDNMYDNLNKNSLS 240	
Db 181 MNPINKLKGTHSKYMEAMYPTKTFPNHHTIVTGLYPESHGIDDNMYDNLNKNSLS 240	
Qy 241 SKENNNPAWHRGQMMWLTAMYQGLKATTYFWPGSEVAINGSFPSIMPYNSVPFEERIS 300	
Db 241 SKENNNPAWHRGQMMWLTAMYQGLKATTYFWPGSEVAINGSFPSIMPYNSVPFEERIS 300	
Qy 301 TLKWLDPKAEPRFYTMFFPBDSSGHAGGPVSARVIKALQVYDHAFGNLMEGIKRN 360	
Db 301 TLKWLDPKAEPRFYTMFFPBDSSGHAGGPVSARVIKALQVYDHAFGNLMEGIKRN 360	
Qy 361 LANCYNTILLADGMDCTYCNKMEYMDYPRINFEYMEGAPTRAHNIPHDEFSNS 420	
Db 361 LANCYNTILLADGMDCTYCNKMEYMDYPRINFEYMEGAPTRAHNIPHDEFSNS 420	
Qy 421 EELVRLSCKPQHFKPMLTPDLPKRLHYANVRIDKVLHFVDQWLAQRSKSNTNCGG 480	
Db 421 EELVRLSCKPQHFKPMLTPDLPKRLHYANVRIDKVLHFVDQWLAQRSKSNTNCGG 480	
Qy 481 GHGYNNEFRSRMBAFIAFLAHPSPKEXTKEVPPENIEVYNLMCDLIAZIOPAINGTHGSLN 540	
Db 481 GHGYNNEFRSRMBAFIAFLAHPSPKEXTKEVPPENIEVYNLMCDLIAZIOPAINGTHGSLN 540	
Qy 541 HLLKVPFYEPSSAEVSKPSVCGFANPLPTESLDCFCPHLONSTQLEQVNOMLNLTQEEI 600	
Db 541 HLLKVPFYEPSSAEVSKPSVCGFANPLPTESLDCFCPHLONSTQLEQVNOMLNLTQEEI 600	
XX SQ Sequence 875 AA;	
XX SQ Best Local Similarity 100.0%; Score 4804; DB 7; Length 875;	

Matches	Conservative	0	Mismatches	0	Indels	0	Gaps	0
Y	1	MESTLTLATEQPYVKNTLKKYKIACTIVIALIYIMMSLGLGLGLGLKLEQGSCREKCFD	60					
Y	1	MESTLTLATEQPYVKNTLKKYKIACTIVIALIYIMMSLGLGLGLGLKLEQGSCREKCFD	60					
Y	61	ASPRGLENCRCDVACKORGDCMDFEDTCVESTRIMNCNKFRCGETRLEASLICSCDDCL	120					
Y	61	ASPRGLENCRCDVACKORGDCMDFEDTCVESTRIMNCNKFRCGETRLEASLICSCDDCL	120					
Y	121	QKDCDACYKSVQGETSWLEENCDTAQSQCPEGFLPPVILFSMDGFRAEYLTYWDTL	180					
Y	121	QKDCDACYKSVQGETSWLEENCDTAQSQCPEGFLPPVILFSMDGFRAEYLTYWDTL	180					
Y	181	MPNTNKLTKTCGTHSKYKRAMYPTKTFPNHYTIVTGYLPESHGIDLNNNNYDYNLNKNSFLS	240					
Y	181	MPNTNKLTKTCGTHSKYKRAMYPTKTFPNHYTIVTGYLPESHGIDLNNNNYDYNLNKNSFLS	240					
Y	241	SKCQNPNPAWWHGQPMWLTAMYQGKKAATYFWPSSEAVINGSPSIIMPYNGSVPFBERIS	300					
Y	241	SKCQNPNPAWWHGQPMWLTAMYQGKKAATYFWPSSEAVINGSPSIIMPYNGSVPFBERIS	300					
Y	301	TLLKWLDPKAERPRFYTMFEEDPSCHAGGPVSVARYIKALQVVDIAFGMIMEGKQRN	360					
Y	301	TLLKWLDPKAERPRFYTMFEEDPSCHAGGPVSVARYIKALQVVDIAFGMIMEGKQRN	360					
Y	361	LHANCVNILLADHGMDDQTYCNKNEYMTDYPRINFYMEGAPRTRAHNTPHDFPSFNS	420					
Y	361	LHANCVNILLADHGMDDQTYCNKNEYMTDYPRINFYMEGAPRTRAHNTPHDFPSFNS	420					
Y	421	EEETVRNLSSRKPKDPIFKYLTDPDLPKRHYAKNVRIXXVHLYFDQOQLAVRSKSNNTNGG	480					
Y	421	EEETVRNLSSRKPKDPIFKYLTDPDLPKRHYAKNVRIXXVHLYFDQOQLAVRSKSNNTNGG	480					
Y	481	GNHGYNNERFSMEAIIPLANGPSFKEKTEVEPPENIETYNNLMDLRLQAPANNIGSLN	540					
Y	481	GNHGYNNERFSMEAIIPLANGPSFKEKTEVEPPENIETYNNLMDLRLQAPANNIGSLN	540					
Y	541	HLLKVPFYEPSHAREVSKEFSCVGPANPLPTESEDCCPHLNQNSTQLEQVNQMLNLTQBEI	600					
Y	541	HLLKVPFYEPSHAREVSKEFSCVGPANPLPTESEDCCPHLNQNSTQLEQVNQMLNLTQBEI	600					
Y	601	TATKVNLFLGRPVLPQKVNDHCLLYHREYVSCFGKAMRPMWSSTYVPOQGDTSPLPPT	660					
Y	601	TATKVNLFLGRPVLPQKVNDHCLLYHREYVSCFGKAMRPMWSSTYVPOQGDTSPLPPT	660					
Y	661	VPDCLRADYRVPSSOKCSFPYLAQDNTHGFLYPASNRTSDSQYDALTISNLVPMYEE	720					
Y	661	VPDCLRADYRVPSSOKCSFPYLAQDNTHGFLYPASNRTSDSQYDALTISNLVPMYEE	720					
Y	721	FRKWDYFHSVLLJKHATERGNYVSPFIDWYDGHFDADDEITKHLANTDVPPTHY	780					
Y	721	FRKWDYFHSVLLJKHATERGNYVSPFIDWYDGHFDADDEITKHLANTDVPPTHY	780					
Y	781	FVLLTSCKNKSHPENCPWLDLVPFIIPHNPINVESEPEGRPEALWVEERTAHARVR	840					
Y	781	FVLLTSCKNKSHPENCPWLDLVPFIIPHNPINVESEPEGRPEALWVEERTAHARVR	840					
Y	841	DVELLTGGLDFYCDKQPYSEILOLKTYLPTFETI	875					
Y	841	DVELLTGGLDFYCDKQPYSEILOLKTYLPTFETI	875					

Db	421	EEIVRNLSCKPDKQHFKPYLTDPLKRYHYAKNVRIDKWHFLVDQOOLAVRSKSNTNCGG	480	CC for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 1 protein of the invention.
Qy	481	GNGYNNEFRSMEAIFIPLAHPSPFEKTEVEPFENTEVVYIMCDLRIQAPENNNGTHGSLN	540	
Db	481	GNGYNNEFRSMEAIFIPLAHPSPFEKTEVEPFENTEVVYIMCDLRIQAPENNNGTHGSLN	540	
Qy	541	HLLKVPFPEPSHAEVSKFSVCGFANPLPTSLDCPFLQHONSTOLEQNMNLTOEEL	600	XX
Db	541	HLLKVPFPEPSHAEVSKFSVCGFANPLPTSLDCPFLQHONSTOLEQNMNLTOEEL	600	SO Sequence 875 AA:
Qy	601	TATVKVNLPGPRVLOKNDLCLLTHREYSGFGRMAMPMWSSVTPQIGDTSPLPPT	660	Query Match 100.0%; Score 4804; DB 7; Length 875;
Db	601	TATVKVNLPGPRVLOKNDLCLLTHREYSGFGRMAMPMWSSVTPQIGDTSPLPPT	660	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	661	VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPASNRTSQDYLITSNLYPMYE	720	Matches 875; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
Db	661	VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPASNRTSQDYLITSNLYPMYE	720	Qy 1 MESTLTLATEQPYKNTLKYKIACTIVILLVIMSLGLGLGLGLKLEKQGCSRKKCFD 60
Qy	721	FRRKWDYHVSVLLKHTERCVNTYSGPITEYNTIGHFADPEITKHLANTDPIPTHY	780	Db 1 MESTLTLATEQPYKNTLKYKIACTIVILLVIMSLGLGLGLGLKLEKQGCSRKKCFD 60
Db	721	FRRKWDYHVSVLLKHTERCVNTYSGPITEYNTIGHFADPEITKHLANTDPIPTHY	780	Qy 61 ASFRGLENCRCDVACKORGDCCDWDFEDTCVESTRIMCNKFRGTYRLEASICSCSDDCL 120
Qy	781	FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNYESCPEGKPEALWVEERFTAHIAVR	840	Db 61 ASFRGLENCRCDVACKORGDCCDWDFEDTCVESTRIMCNKFRGTYRLEASICSCSDDCL 120
Db	781	FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNYESCPEGKPEALWVEERFTAHIAVR	840	Qy 121 QKDDCADYKSVCOGETSWLEENCDTAQSQCPEGFLPPVILFSMDGFRAYLYTWDTL 180
Qy	841	DVELLTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875	9	Db 121 QKDDCADYKSVCOGETSWLEENCDTAQSQCPEGFLPPVILFSMDGFRAYLYTWDTL 180
Db	841	DVELLTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875	9	Qy 181 MPNINKLKLTCGIESKVNMEAMYPTKTFPHYITVPTGYPESHGTIDNMYDYNLNKNFSL 240
Qy	841	DVELLTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875	9	Db 181 MPNINKLKLTCGIESKVNMEAMYPTKTFPHYITVPTGYPESHGTIDNMYDYNLNKNFSL 240
Db	841	DVELLTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875	9	Qy 241 SKEQNPAWNGQDGMILTYQCLKAATYFWGSEAVINGSPPSITMPYNGSVPFERRIS 300
Qy	241	SKEQNPAWNGQDGMILTYQCLKAATYFWGSEAVINGSPPSITMPYNGSVPFERRIS 300	9	Db 241 SKEQNPAWNGQDGMILTYQCLKAATYFWGSEAVINGSPPSITMPYNGSVPFERRIS 300
Db	301	TLIKWLDLPAERPRFXTMYFEEPDSSGHAGGPVSARVITALQVNDHAFGMLMEGLKQRN	360	Qy 301 TLIKWLDLPAERPRFXTMYFEEPDSSGHAGGPVSARVITALQVNDHAFGMLMEGLKQRN 360
Db	301	TLIKWLDLPAERPRFXTMYFEEPDSSGHAGGPVSARVITALQVNDHAFGMLMEGLKQRN	360	Db 301 TLIKWLDLPAERPRFXTMYFEEPDSSGHAGGPVSARVITALQVNDHAFGMLMEGLKQRN 360
Qy	361	LHNCVNTILLADHGMDQTYCNRNEYMDYFPRINFYMEGAPRRAHNTPHDFPSFNS	420	Qy 361 LHNCVNTILLADHGMDQTYCNRNEYMDYFPRINFYMEGAPRRAHNTPHDFPSFNS 420
Db	361	LHNCVNTILLADHGMDQTYCNRNEYMDYFPRINFYMEGAPRRAHNTPHDFPSFNS	420	Db 361 LHNCVNTILLADHGMDQTYCNRNEYMDYFPRINFYMEGAPRRAHNTPHDFPSFNS 420
Qy	421	EEIVRNLSCKRKPFQHFKPYLTDPLPKRLHYAKNVRIDKVKHLFDQOQLAVRSKSNTNCGG	480	Qy 421 EEIVRNLSCKRKPFQHFKPYLTDPLPKRLHYAKNVRIDKVKHLFDQOQLAVRSKSNTNCGG 480
Db	421	EEIVRNLSCKRKPFQHFKPYLTDPLPKRLHYAKNVRIDKVKHLFDQOQLAVRSKSNTNCGG	480	Db 421 EEIVRNLSCKRKPFQHFKPYLTDPLPKRLHYAKNVRIDKVKHLFDQOQLAVRSKSNTNCGG 480
Qy	481	GNHGYNNERFSMELFLAHGSPSKKEVEEPENNTYINLMCDLRLQAPAPNGTGSLN	540	Qy 481 GNHGYNNERFSMELFLAHGSPSKKEVEEPENNTYINLMCDLRLQAPAPNGTGSLN 540
Db	481	GNHGYNNERFSMELFLAHGSPSKKEVEEPENNTYINLMCDLRLQAPAPNGTGSLN	540	Db 481 GNHGYNNERFSMELFLAHGSPSKKEVEEPENNTYINLMCDLRLQAPAPNGTGSLN 540
Qy	541	HLLKVPFYPEPSHAEVSKFSVCCFANPLPTESLDCFCPHLNQSTOLEQVNQMLNLQEEL	600	Qy 541 HLLKVPFYPEPSHAEVSKFSVCCFANPLPTESLDCFCPHLNQSTOLEQVNQMLNLQEEL 600
Db	541	HLLKVPFYPEPSHAEVSKFSVCCFANPLPTESLDCFCPHLNQSTOLEQVNQMLNLQEEL	600	Db 541 HLLKVPFYPEPSHAEVSKFSVCCFANPLPTESLDCFCPHLNQSTOLEQVNQMLNLQEEL 600
Qy	601	TATVKVNLPGFGRPTVQLRNDVHCLLTHREYSGFGRMAMPMWSSVTPQLDTSPLPPT	660	Qy 601 TATVKVNLPGFGRPTVQLRNDVHCLLTHREYSGFGRMAMPMWSSVTPQLDTSPLPPT 660
Db	601	TATVKVNLPGFGRPTVQLRNDVHCLLTHREYSGFGRMAMPMWSSVTPQLDTSPLPPT	660	Db 601 TATVKVNLPGFGRPTVQLRNDVHCLLTHREYSGFGRMAMPMWSSVTPQLDTSPLPPT 660
Qy	661	VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPSNTFSDSQDALITSNLYPMYE	720	Qy 661 VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPSNTFSDSQDALITSNLYPMYE 720
Db	661	VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPSNTFSDSQDALITSNLYPMYE	720	Db 661 VPDCLRADVRVPSESOCSFYLADKNITHGFLYPPSNTFSDSQDALITSNLYPMYE 720
Qy	721	FRKWDYHVSLLKHTERGVNTSGP1DNYDHFDADPEITKHLANTDVP1PTHY	780	Qy 721 FRKWDYHVSLLKHTERGVNTSGP1DNYDHFDADPEITKHLANTDVP1PTHY 780
Db	721	FRKWDYHVSLLKHTERGVNTSGP1DNYDHFDADPEITKHLANTDVP1PTHY	780	Db 721 FRKWDYHVSLLKHTERGVNTSGP1DNYDHFDADPEITKHLANTDVP1PTHY 780
Qy	781	FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNVSCEPGXPEALWVEERFTAHARVR	840	Qy 781 FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNVSCEPGXPEALWVEERFTAHARVR 840
Db	781	FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNVSCEPGXPEALWVEERFTAHARVR	840	Db 781 FVVLTSCKNKSHTPENCQWLDLPTIIPHRPTNVSCEPGXPEALWVEERFTAHARVR 840
Qy	841	DVELTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI	875	Qy 841 DVELTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875
Db	841	DVELTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI	875	Db 841 DVELTGIDFYQDKVQPSVSEIQLQKTYLPTFETTI 875

ADE65984	ID ADE65984 standard; protein; 875 AA.	XX	Db 301 TLLKNDLPAERPRFTYMFEEPSGHAGGPASARTIKALQVDHAGMIMEGLKORN 360
ADE65984;		XX	Qy 361 LHNQCNVNIILLADHGMDQTYOKMRYMTDFPRINFFYMYEGPAPIRAHNIPHDFFNSN 420
AC		XX	Db 361 LHNQCNVNIILLADHGMDQTYOKMRYMTDFPRINFFYMYEGPAPIRAHNIPHDFFNSN 420
DT	29-JAN-2004 (first entry)	XX	Qy 421 EEEIVNLSCRKPDQHKPVLTPDLPKRLHYAKNTRIDKYLFDQMLAVRSKSNTNCGG 480
DE	Human 161P2F10B protein variant 6 #3.	XX	Db 421 EEEIVNLSCRKPDQHKPVLTPDLPKRLHYAKNTRIDKYLFDQMLAVRSKSNTNCGG 480
KW	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.	XX	Qy 481 GNHGYNNEFESMEALFLAHPSPFKEKTEVPPFENIEVNLMDLRLIQAPNINGTHGSIN 540
OS	Homo sapiens.	XX	Db 481 GNHGYNNEFESMEALFLAHPSPFKEKTEVPPFENIEVNLMDLRLIQAPNINGTHGSIN 540
OS	W02003040340-A2.	XX	Qy 541 HLLKVPFYEPSSHAEEVSKFSCVGPANPLPESLJCFCPHLQNSTOLEQVNONMLTQEEL 600
PD	15-MAY-2003.	XX	Db 541 HLLKVPFYEPSSHAEEVSKFSCVGPANPLPESLJCFCPHLQNSTOLEQVNONMLTQEEL 600
PF	07-NOV-2002; 2002WO-US036002.	XX	Qy 601 TATVKVNLPGFRPRVYPLQKNDHCLYLHREYVSGTGKANRMPMMSYYTVPQLGDTSPLPPT 660
PF	07-NOV-2001; 2001US-00005480.	XX	Db 601 TATVKVNLPGFRPRVYPLQKNDHCLYLHREYVSGTGKANRMPMMSYYTVPQLGDTSPLPPT 660
PR	31-JAN-2002; 2002US-00062109.	XX	Qy 661 VPDCLRADYRVPSPSQKSFSYFLADKNTTHGFLYPPASNRTSDSQYDALTISNLVPMYEE 720
PR	(AGEN-) AGENSYS INC.	XX	Db 661 VPDCLRADYRVPSPSQKSFSYFLADKNTTHGFLYPPASNRTSDSQYDALTISNLVPMYEE 720
PI	Jacobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;	XX	Qy 721 FRYKWDYFHSVLLIKAHATERGVNVNSGP1FDNYDGHEDAPDITKHANTDPIPTY 780
PI	Morrison RK, Challita-Eid PM;	XX	Db 721 FRYKWDYFHSVLLIKAHATERGVNVNSGP1FDNYDGHEDAPDITKHANTDPIPTY 780
PI	WPI; 2003-441560/41.	XX	Qy 781 FVVLTSCKNKSHTPENCPGMWLDVLPFIPHRPTVESPCEPGKPAWBERFTAHIAVR 840
PT	A composition for diagnosing, preventing and treating cancer (e.g. PT	XX	Db 781 FVVLTSCKNKSHTPENCPGMWLDVLPFIPHRPTVESPCEPGKPAWBERFTAHIAVR 840
PT	prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides	XX	Qy 841 DVELLTGDFYQDKYTOPVSEIQLQRTYLPFTETI 875
PT	and polypeptides.	XX	Db 841 DVELLTGDFYQDKYTOPVSEIQLQRTYLPFTETI 875
PT	Example 5; SEQ ID NO 96; 135pp; English.	XX	RESULT 11
XX	This invention relates to a novel composition which comprises a substance	CC	ID ADE65991 standard; protein; 875 AA.
CC	that modulates the status of a novel protein (161P2F10B) and its variants	CC	XX
CC	having 875 amino acids provided in the specification. The	CC	XX
CC	protein of the invention is over-expressed in certain cancers. The	CC	XX
CC	compounds of the invention may have cytostatic activity and the sequence	CC	XX
CC	of the 161P2F10B protein, and the gene which encodes it, may be useful	CC	XX
CC	for gene therapy or the development of a vaccine. The composition and	CC	XX
CC	methods of the invention are useful in diagnosing, preventing and	CC	XX
CC	treating cancer. The present sequence is the amino acid sequence of the	CC	XX
CC	human 161P2F10B variant 6 protein of the invention.	CC	XX
XX	Sequence 875 AA;	XX	DT 29-JAN-2004 (first entry)
SQ	Query Match 100.0%; Score 4804; DB 7; Length 875;	XX	XX Human 161P2F10B protein variant 1 #6.
Best Local Similarity 100.0%; Pred. No. 0;	Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
Qy	1 MESTITLATEQPKKNTLKKYKICIVLLALYIMSLGIGLGLRLEKQGSCRKCFD 60	XX	XX Homo sapiens.
Db	1 MESTITLATEQPKKNTLKKYKICIVLLALYIMSLGIGLGLRLEKQGSCRKCFD 60	XX	XX WO2003040340-A2.
Qy	61 ASFRGLENCCDVACKDRGDCWDEDTCEVSTRMCNKFRGCTEASLSCSDCL 120	XX	XX 15-MAY-2003.
Db	61 ASFRGLENCCDVACKDRGDCWDEDTCEVSTRMCNKFRGCTEASLSCSDCL 120	XX	XX 07-NOV-2002; 2002WO-US036002.
Qy	121 QKKDCCADYKSVCGQETSNLBEENDCTAQOSQCPGEFLDLPVILFMSMDGFRAEYLWTDL 180	XX	XX (AGEN-) AGENSYS INC.
Db	121 QKKDCCADYKSVCGQETSNLBEENDCTAQOSQCPGEFLDLPVILFMSMDGFRAEYLWTDL 180	XX	XX 07-NOV-2001; 2001US-00005480.
Qy	181 MPNINKLTKTCIHSKMRAMYPTKTPHMYITVGLYPHSGHIDNNMYDVNLNKNSLS 240	XX	XX 31-JAN-2002; 2002US-00062109.
Db	181 MPNINKLTKTCIHSKMRAMYPTKTPHMYITVGLYPHSGHIDNNMYDVNLNKNSLS 240	XX	XX PR PA
Qy	241 SKEQNNPAWQGPMULTAMYQGLKATWFGPSEVATINGSFSIYMPYNGSYPFERIS 300	XX	XX (AGEN-) AGENSYS INC.
Db	241 SKEQNNPAWQGPMULTAMYQGLKATWFGPSEVATINGSFSIYMPYNGSYPFERIS 300	XX	XX 07-NOV-2002; 2002WO-US036002.
Qy	301 TLLKNDLPAERPRFTYMFEEPSGHAGGPASARTIKALQVDHAGMIMEGLKORN 360	XX	XX PR PA

Db	601 TATVKVNLPFFGRPRVQKVDHCLLYHREYVSGFCKAVMPMNSSTVPLQGDTSP1PPT	60	Qy	1 MESTLILATEPVEKNTLKYKIACTIVLALLVIMSGLIGLGLRLKQGSRKCKCFD	60
Qy	661 VPDCLRADYRVPSSQCSFYLADKNTTHFLYPPASRTSDSOYDALITSNLVPNTE	720	Db	1 MESTLILATEPVEKNTLKYKIACTIVLALLVIMSGLIGLGLRLKQGSRKCKCFD	60
Db	661 VPDCLRADYRVPSSQCSFYLADKNTTHFLYPPASRTSDSOYDALITSNLVPNTE	720	Qy	61 ASFRGLENCRDVAKCDRGDCWDFDTCEVESTRIMCNKFRGCTERLEASLCSDDCL	120
Qy	721 FRKWDYFPIVSLLIKHATERNGVNVSGI1FDNYDGHFADPDTKHLANTDVP1PHTY	780	Db	61 ASFRGLENCRDVAKCDRGDCWDFDTCEVESTRIMCNKFRGCTERLEASLCSDDCL	120
Db	721 FRKWDYFPIVSLLIKHATERNGVNVSGI1FDNYDGHFADPDTKHLANTDVP1PHTY	780	Qy	121 QKDCDCADYKSVQCGETSWSLEENCDTAQOSQCPEGFDLPPVTLFSMDGFRAEYLTYTDTL	180
Qy	781 FVVLTSCKRKSHTPENCPGWLDPFLPIHRPTVNECPEGKPEALWVEERTAHTARV	840	Db	121 QKDCDCADYKSVQCGETSWSLEENCDTAQOSQCPEGFDLPPVTLFSMDGFRAEYLTYTDTL	180
Db	781 FVVLTSCKRKSHTPENCPGWLDPFLPIHRPTVNECPEGKPEALWVEERTAHTARV	840	Qy	181 MPNINKLKTGCGIHSKYMRAAMYPTKTFPHNTYITGLYBPSHGLIDNNMYDVLNKNSIS	240
Qy	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875	Db	181 MPNINKLKTGCGIHSKYMRAAMYPTKTFPHNTYITGLYBPSHGLIDNNMYDVLNKNSIS	240
Db	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875	Qy	241 SKEQNNPAWTHGQPMWLTAMYQGKKAATYFWSSEVAINGSPPS1TNPYNGSYPFEBRIS	300
Db	RES1T 14		Db	241 SKEQNNPAWTHGQPMWLTAMYQGKKAATYFWSSEVAINGSPPS1TNPYNGSYPFEBRIS	300
ADB65893	ADB65893 standard; protein; 875 AA.		Qy	301 TLLKWLDPKAERPRFTYMEPEPDSSHAGGPVSAVTKALQVVDAGMELMEGJKQRN	360
ID	ADB65893 standard; protein; 875 AA.		Db	301 TLLKWLDPKAERPRFTYMEPEPDSSHAGGPVSAVTKALQVVDAGMELMEGJKQRN	360
XX			Qy	361 LHNCVNILLIADHGMDQTYCNCMEYMTDFPRINFFYMEGAPTRAHN1PHDFFEFNS	420
AC			Db	361 LHNCVNILLIADHGMDQTYCNCMEYMTDFPRINFFYMEGAPTRAHN1PHDFFEFNS	420
XX	29-JAN-2004 (first entry)		Qy	421 EETIVRNLSCKRKDQHFKPFLTPDLPKRLHYAKNRIDKVLFYDQOWLAVRSKSNTNCGG	480
DE	Human 161P2F10B protein variant 2.		Db	421 EETIVRNLSCKRKDQHFKPFLTPDLPKRLHYAKNRIDKVLFYDQOWLAVRSKSNTNCGG	480
XX	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.		Qy	481 GHGYNNRFRSMEAIFLAHGPSFKEKTEVEPENIENVYLNCDLRLIQPAPNGTGSLN	540
XX	Homo sapiens.		Db	481 GHGYNNRFRSMEAIFLAHGPSFKEKTEVEPENIENVYLNCDLRLIQPAPNGTGSLN	540
OS			Qy	541 HLLKVPYEPSPHAEEVSKFSEVGFANLPTESSLDCPCPHLONSTOLEQVNQMLNLTOEEI	600
XX	WO2003040340-A2.		Db	541 HLLKVPYEPSPHAEEVSKFSEVGFANLPTESSLDCPCPHLONSTOLEQVNQMLNLTOEEI	600
XX	15-MAY-2003.		Qy	601 TATVKVNLPFGPRTQKNDHCLLYREYVSGFGKAMRPMWSSYTPQLGDTSP1PPT	660
PD			Db	601 TATVKVNLPFGPRTQKNDHCLLYREYVSGFGKAMRPMWSSYTPQLGDTSP1PPT	660
XX	07-NOV-2002; 2002WO-US0360002.		Qy	661 VPDCLRADVVPSESSQCSFYLADKNTTHFLYPPASRTSDCYDLSQDALTISNLYPMYE	720
PP			Db	661 VPDCLRADVVPSESSQCSFYLADKNTTHFLYPPASRTSDCYDLSQDALTISNLYPMYE	720
XX	07-NOV-2001; 2001US-00005480.		Qy	721 FRKWDYFHSVLLIKHATERGVNVSGGPFDYNTDGHFDAPDELTKHLANTDVP1PHTY	780
PR			Db	721 FRKWDYFHSVLLIKHATERGVNVSGGPFDYNTDGHFDAPDELTKHLANTDVP1PHTY	780
XX	31-JAN-2002; 2002US-00062109.		Qy	781 FVVLTSCKRKSHTPENCPGWLDPFLPIHRPTVNECPEGKPEALWVEERTAHARYR	840
PA	(AGEN-) AGENSYS INC.		Db	781 FVVLTSCKRKSHTPENCPGWLDPFLPIHRPTVNECPEGKPEALWVEERTAHARYR	840
XX	Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KJM;		Qy	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875
PI	PI: 2003-441560/41.		Db	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875
PI	Morrison RK, Chalilca-Eid PM;		Qy	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875
XX	DR: AD655892.		Db	841 DVELLTGGLDFQDKVQPVSEIOLKTYLPTFETTI	875
XX	XX		Qy	RESULT 15	
PT	A composition for diagnosing, preventing and treating cancer (e.g. prostate, renal or uterine cancer) comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants.		Db	ID ADE65897 standard; protein; 875 AA.	
PT	polypeptides.		Qy	XX	
XX	Claim 1; SEQ ID NO 5; 135pp; English.		Db	XX	
XX	This invention relates to a novel composition which comprises a substance that modulates the status of a novel protein (161P2F10B) and its variants having a sequence of 875 amino acids provided in the specification. The protein of the invention is over-expressed in certain cancers. The compounds of the invention may have cytostatic activity and the sequence of the 161P2F10B protein, and the gene which encodes it, may be useful for gene therapy or the development of a vaccine. The composition and methods of the invention are useful in diagnosing, preventing and treating cancer. The present sequence is the amino acid sequence of the human 161P2F10B variant 2 protein of the invention.		AC ADE65897;		
CC	Sequence 875 AA;		XX	XX	
CC	Query Match 99.9%; Score 4801; DB 7; Length 875;		XX	XX	
CC	Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Gaps 0;		XX	XX	
CC	Matches 874; Conservative 1; Gaps 0;		XX	XX	
CC	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.		XX	XX	
SQ	29-JAN-2004 (first entry)		DT		

OS Homo sapiens.
 XX WO2003040340-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US036002.
 XX
 PR 07-NOV-2001; 2001US-00005480.
 PR 31-JAN-2002; 2002US-00062109.
 XX
 (AGEN-) AGENSY INC.
 XX Jakobovits A, Raitano AB, Faris M, Hubert RS, Ge W, Morrison KM;
 PI Morrison RK, Chaillita-Eid PM;
 XX WPI; 2003-441560/41.
 DR -N-PSDB; AD65896.
 XX
 PT A composition for diagnosing, preventing and treating cancer (e.g.
 PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
 PT and polypeptides.
 XX SEQ ID NO 9; 135pp; English.
 PS
 CC This invention relates to a novel composition which comprises a substance
 CC that modulates the status of a novel protein (161P2F10B) and its variants
 CC having a sequence of 875 amino acids provided in the specification. The
 CC protein of the invention is over-expressed in certain cancers. The
 CC compounds of the invention may have cytostatic activity and the sequence
 CC of the 161P2F10B protein, and the gene which encodes it, may be useful
 CC for gene therapy or the development of a vaccine. The composition and
 CC methods of the invention are useful in diagnosing, preventing and
 CC treating cancer. The present sequence is the amino acid sequence of the
 CC human 161P2F10B variant 4 protein of the invention.
 XX Sequence 875 AA;

Query Match 99.9%; Score 4798; DB 7; Length 875;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 874; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MESTLTLATEQPYKNTLKKYKIACTIVLALLIVMSIGLGLGLGLRKLKEQGSCREKCFD 60
 DB 1 MESTLTLATEQPYKNTLKKYKIACTIVLALLIVMSIGLGLGLGLRKLKEQGSCREKCFD 60

QY 61 ASPLGLENCRCDYACKDGDCCWDFDENTCVESTRIMNKFCGETRLEASLCSCSDDCL 120
 DB 61 ASPLGLENCRCDYACKDGDCCWDFDENTCVESTRIMNKFCGETRLEASLCSCSDDCL 120

QY 121 QKDCCADAKYSVCGETSMLEENCDTAQSQCPEGFDLPPVILFSMDGFRAYLYWDTL 180
 DB 121 QKDCCADAKYSVCGETSMLEENCDTAQSQCPEGFDLPPVILFSMDGFRAYLYWDTL 180

QY 181 MPNINKLKGIGIHKYMRAMYPTKTFPMYTITVGLYFESHLGLIDNNMDVLNKNFSL 240
 DB 181 MPNINKLKGIGIHKYMRAMYPTKTFPMYTITVGLYFESHLGLIDNNMDVLNKNFSL 240

QY 241 SKEONNPAPWHPGPNWLTAMYQGKAAATFWPGSEVAINGSSEPPSIYMPYNGSVPFERIS 300
 DB 241 SKEONNPAPWHPGPNWLTAMYQGKAAATFWPGSEVAINGSSEPPSIYMPYNGSVPFERIS 300

QY 301 TLLKWLDPKAERPRFYTMYFEEPDSSGHAGGPVSAVTAKALQYDHFQWMAVRSKSNTNGG 360
 DB 301 TLLKWLDPKAERPRFYTMYFEEPDSSGHAGGPVSAVTAKALQYDHFQWMAVRSKSNTNGG 360

QY 361 LHNCVNILLADHGMDQTYCNKMEYMTDYPYRINFFYMEGAPRIRAHNIPDFFESNS 420
 DB 361 LHNCVNILLADHGMDQTYCNKMEYMTDYPYRINFFYMEGAPRIRAHNIPDFFESNS 420

QY 421 EEEVNLNSCRPDQHFKPYLTPDLPKRLHYAKNVRIDKVLFDQWMAVRSKSNTNGG 480
 DB 421 EEEVNLNSCRPDQHFKPYLTPDLPKRLHYAKNVRIDKVLFDQWMAVRSKSNTNGG 480

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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:17:02 ; Search time 23 Seconds
 (without alignments)

1964.032 Million cell updates/sec

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTLTLATEQPVKNTLKK.....QPVSEILQLKTYLPTFETTI 875

Scoring table: BLOSUM62

GapcP 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgcn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgcn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgcn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgcn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgcn2_6/ptodata/2/iaa/PECTUS_COMB.pep:*

6: /cgcn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2498.5	52.0	873	3 US-09-187-331-6	Sequence 6, Appli
2	2498.5	52.0	873	4 US-09-470-946-6	Sequence 6, Appli
3	2498.5	52.0	873	4 US-09-433-906-2	Sequence 2, Appli
4	2498.5	52.0	925	2 US-08-392-946-1	Sequence 1, Appli
5	2498.5	52.0	925	2 US-08-501-169-1	Sequence 1, Appli
6	2498.5	52.0	900	1 PCT-US94-14893-1	Sequence 1, Appli
7	2494.5	51.9	873	4 US-09-430-906-4	Sequence 4, Appli
8	2040.5	42.5	915	1 US-08-346-455B-69	Sequence 69, Appli
9	2040.5	42.5	915	4 US-08-977-221-69	Sequence 69, Appli
10	2040.5	42.5	915	4 US-09-483-831B-34	Sequence 69, Appli
11	2040.5	42.5	915	5 PCT-US95-06613-69	Sequence 69, Appli
12	1964.5	40.9	829	3 US-08-346-455B-34	Sequence 34, Appli
13	1964.5	40.9	829	3 US-08-977-221-34	Sequence 34, Appli
14	1964.5	40.9	829	4 US-09-483-831B-34	Sequence 34, Appli
15	1964.5	40.9	829	5 PCT-US95-06613-34	Sequence 34, Appli
16	1923.5	40.0	861	1 US-09-346-455B-67	Sequence 67, Appli
17	1923.5	40.0	861	3 US-08-977-221-67	Sequence 67, Appli
18	1923.5	40.0	861	4 US-09-483-831B-67	Sequence 67, Appli
19	1923.5	40.0	861	5 PCT-US95-06613-67	Sequence 67, Appli
20	1838.5	38.3	979	1 US-08-346-455B-38	Sequence 38, Appli
21	1838.5	38.3	979	3 US-08-977-221-39	Sequence 38, Appli
22	1838.5	38.3	979	4 US-09-483-831B-70	Sequence 70, Appli
23	1838.5	38.3	979	5 PCT-US95-06613-38	Sequence 38, Appli
24	1761.5	36.7	788	1 US-08-346-455B-36	Sequence 36, Appli
25	1761.5	36.7	788	3 US-08-977-221-36	Sequence 36, Appli
26	1761.5	36.7	788	4 US-09-483-831B-36	Sequence 36, Appli
27	1761.5	36.7	788	5 PCT-US95-06613-36	Sequence 36, Appli

ALIGNMENTS

RESULT 1
 US-09-187-331-6
 ; Sequence 6, Application US-09187331
 ; General Information:
 ; Applicant: Yue, Henry
 ; Applicant: Corley, Neil C.
 ; Applicant: Guegler, Karl C.
 ; Applicant: Gorgone, Gina A.
 ; Applicant: Baugh, Mariah R.
 ; Title of Invention: Cell Surface Glycoproteins
 ; File Reference: PE-0631 US
 ; Current Application Number: US-09/187-331
 ; Sequence ID: NO 6
 ; SEQ ID NO 6
 ; LENGTH: 873
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: -
 ; OTHER INFORMATION: 9189650
 US-09-187-331-6

Query Match 52.0% ; Score 2498.5 ; DB 3 ; Length 873;
 Best Local Similarity 53.1% ; Pred. No. 8e-235;
 Matches 465 ; Conservative 137 ; Mismatches 250 ; Indels 23 ; Gaps 11;

QY 10 EQPVKK----KYKTAIVVALLVIMSIGGLGLIRKLEQGSCRKKCFCFDAS 62
 5 EEPPEKAARAAARTAKDPTVYKVLISVSVVITLICIFGKPKPSKCKGCRFERT 64
 DB 123 KDCADAKYKSVQCGETSMILEENCDTAQSQCPREGFDLPPVILFSMUGFRAYLYTDTIMP 182
 122 GDCCIINSSVQCGEKSMEPECESTINEPOCPAGFETPTPLFSLQGRABYLHTWGGLLP 181
 65 F---GNCRCDAACTELNCCLDQYQETDIEPHWINTNKFCGEKRLTRSCACSDCRDK 121
 QY 123 NINKLKTCGTHSKYKMRAMYPIKTFPNHYTIVGLYFESHLGIDNNYYDVNLNQFSLSSK 242
 DB 182 VSKLKKCGTGYTKNMREVYPTKTFPHYSIVTGVLYFESHGIDDNKMYDPKRNASFLSK 241
 QY 243 BQNPAPWPHGQQPWLMTAMYQGLRAATYFWPGSEEVANGSFPSYNGSVPFEERISTL 302
 DB 242 EKRNPEWYKGEPWATKYGQKSGCFFWPSSDVEINGIPDIIYKOMYNGSVPFEEILLAV 301
 QY 303 LKWLDPKAERFRFTMYFEEFDSSHAGGIVSARVIAKLVQVDFAGMLMEGLQRNLH 362

Db 302 LQWLOLPKDERPHFTLYLEPDSGHSYGPYSESEVIALQRVGMYGMLMDGLKEINLH 361
 Qy 363 NCVNILLADHMDDOTYCNKMEYMTDYPRINFFYMEYEGPAPRIRAINPHDFFENSEE 422
 Db 362 RCLNLILISDPMGEGQGSCCKYIYLKVLGDVNKNIKVYGAARLRSVDPCYCSENYEG 421
 Qy 423 IVRNLSCREPDOHFKPVLTPDLSKRLHYAKNTYRDLVHFLDQW-LAVRSKSNTNCGG 481
 Db 422 IARNLSCREPNOHKPVLTPDLSKRLHYAKNTYRDLVHFLDQWQALANLNSERKYCGSG 481
 Qy 482 NHGYNNEFSSMEA-PLAAGPSFKEKTEVPEFENIEVNLNCDMLLRLTOPAPNGTHGSLNH 541
 Db 482 FHGSNDNVFENMQALFVGCGFPKFGTEADTFENIEVNLNCDMLLNLTPAPNGTHGSLNH 541
 Qy 542 LLKXPFYEEPSHAEEVSKFSSVCGFANPLPTEISLDCFC- PHLNQSTOLEQVNQMLNLTQEELI 600
 Db 542 LLKXNPVYTHPKHPEVHPLVQCPPTRN- PRDNLGCSNCNPSTI -- LP1EDFQTQFNLTVAEE 597
 Qy 601 TATVKVNLLFGRPVLOVQDNVHCLLYREYYVGFGRAMRPNKWSSTYVPLQGDTSPLPPT 660
 Db 598 KLIKHETIYGRPVLQKENTICLLSQHFMGYSQDILMPWTSVTVDR -NDFSESTD 655
 Qy 651 VPDCLRAVYRVPSESESQCSFYLADKNITHGFLYPPDASRNTSDQY- DALITSNLYPMYE 719
 Db 656 FSNQLYQDFRIPSLPVHCCSFYKNTVSYGFLSPQLNKNSSGTYSEALLTNTIVPMYQ 715
 Qy 720 EPRKMDYDFHSVSLIKHATERGVNTVYSGPFDYNYDGHFDAPDETKH -- LANTDVP1 776
 Db 716 SFQVITWRYFHDTLRLCYAERGVNTVYSGPFDYDFGRCDSLLENLRKERVIRNQELLI 775
 Qy 777 PTHXPFULTSCKNSKHPENCGWLDLPIIPHRTINVECSPEGPEAWVVEERFTAH1 836
 Db 776 PTHFFVILTSCKDTSQPLHCEN-LDTLAFILPHRTDNNSESCVHGKHDSSWELLMLHR 834
 Qy 837 ARVRDVEELTGLDFYQDKVQPVSEIQLQKTYLPTF 871
 Db 835 ARITDVEHITGSLSFYQKREPVSDIQLKJLPTF 869
 Qy 601 TATVKVNLLFGRPVLOVQDNVHCLLYREYYVGFGRAMRPNKWSSTYVPLQGDTSPLPPT 660
 Db 598 KLIKHETIYGRPVLQKENTICLLSQHFMGYSQDILMPWTSVTVDR -NDFSESTD 655
 Qy 661 VPDCRLADVRVPSESESQCSFYLADKNITHGFLYPPDASRNTSDQY-DALITSNLYPMYE 719
 Db 656 FSNQLYDFRIPSLPVHCCSFYKNTVSYGFLSPQLNKNSSGTYSEALLTNTIVPMYQ 715
 Qy 720 EPRKMDYDFHSVSLIKHATERGVNTVYSGPFDYNYDGHFDAPDETKH -- LANTDVP1 776
 Db 716 SFQVITWRYFHDTLRLCYAERGVNTVYSGPFDYDFGRCDSLLENLRKERVIRNQELLI 775
 Qy 777 PTHXPFULTSCKNSKHPENCGWLDLPIIPHRTINVECSPEGPEAWVVEERFTAH1 836
 Db 776 PTHFFVILTSCKDTSQPLHCEN-LDTLAFILPHRTDNNSESCVHGKHDSSWELLMLHR 834
 Qy 837 ARVRDVEELTGLDFYQDKVQPVSEIQLQKTYLPTF 871
 Db 835 ARITDVEHITGSLSFYQKREPVSDIQLKJLPTF 869

RESULT 2
 US-09-470-946-6
 ; Sequence 6, Application US/09470946
 ; Patent No. 6318923

; GENERAL INFORMATION:
 ; APPLICANT: Rue, Henry
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Gorgone, Gina A.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: CELL SURFACE GLYCOPROTEINS
 ; CURRENT APPLICATION NUMBER: US/09/470,946
 ; CURRENT FILING DATE: 1999-12-22
 ; EARLIER APPLICATION NUMBER: US 09/187,331
 ; EARLIER FILING DATE: 1998-11-06
 ; NUMBER OF SEQ ID NOS: 6
 ; SEQ ID NO: 6
 ; LENGTH: 873
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: 9189650

Query Match 52.0% ; Score 2498.5; DB 4; Length 873;
 Best Local Similarity 53.1%; Pred. No. 8e-235; Indels 23; Gaps 11;
 Matches 465; Conservative 13; Mismatches 250;

Qy 10 EOPVKE----NTLK---KYKACIYVLLALLIVMSIGLIGLGLRKLEKQGSKRKCDAS 62
 Db 5 EEPLEKAARRARTAKDNTYKVLISVLSVCLTTLGCFGLKXPSCAKEVKSCGKRCFPT 64

RESULT 3
 US-09-438-906-2
 ; Sequence 2, Application US/09438906
 ; Patent No. 6665185

; GENERAL INFORMATION:
 ; APPLICANT: Goldfine, Ira
 ; APPLICANT: Trischitta, Vincenzo
 ; APPLICANT: Pizzutti, Antonio
 ; APPLICANT: Vigheri, Riccardo
 ; APPLICANT: Frittitta, Lucia
 ; TITLE OF INVENTION: Polymorphic Human PC-1 Sequences
 ; FILE REFERENCE: 9076-089
 ; CURRENT APPLICATION NUMBER: US/09/438,906
 ; CURRENT FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 60/108,853
 ; PRIOR FILING DATE: 1998-11-18

NUMBER OF SEQ ID NOS: 35
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 873
 TYPE: PRT
 ORGANISM: H. sapiens
 US-09-438-906-2

Query Match 52.0%; Score 2498.5; DB 4; Length 873;
 Best Local Similarity 53.1%; Pred. No. 8e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EQPVYK---NTLK---KYKACIVLALLVINSILGUGLGLRKCEKGQSPRKCKEDAS 62
 Db 5 EPELEKAARARTAXDNTPKVLSVILSVCVLTILGKPKSCAREVKSKGRFERT 64

Qy 63 ERGLENCEKCDVACKDGRGDFCWDPEDTCYESTRWMCNKFRCGTRILASLCSDDQIOK 122
 Db 65 F---GNCRCDAACTVGLNCLDQETCCEPEHWTNCNPKRCGEKRLTRSLCAGCSDDCKDK 121

Qy 123 KDCCADYKSVCOGETSWLEENCDAQOQSCCPGFDLPPVILFMDGPRAEYLTTWDTLMP 182
 Db 122 GDCCINYYSSVCOGKRSWEPCEINEPOCPAEPETPTLFLDGPRAEYLHTWGGLP 181

Qy 183 NINKLKTCTGITHSKYMRKAMYPTKTPPNHHTVLTGYPESHGIDDNMMYDNLNKNFESLSK 242
 Db 182 VISLKKKCGCTYTKMRPYPPTKTPPNHHTVLTGYPESHGIDDNMMYDNLNKNFESLSK 241

Qy 243 EQNPAWNGQPKWLTAMQOGLRATYTFPQGSEVAINSSFPSPYMPNGSVFPEERISTL 302
 Db 242 EKENPEWYKGEPIPAWTKYQGLSGTFFWPGSDVEINGFPDLYKMYNGSVFPEERILAV 301

Qy 303 LKWLDPKAERPRFETYMFEEPDSSGHAGGPVSAVIRAKQVVDHAFRMGLKGRLKORNHL 362
 Db 302 LQWLQLPKPERPHTFTLKEEDPSGSHTGPVSEVIALQVLDGMYCMLMQLKELNHL 361

Qy 363 NCVNILLADHGMDOTYCNKMEYNTDYPFRINPFYMMGPPAPRIMHIDHOFFSENSE 422
 Db 362 RCLNLLJLISHGMEGSKCKYIYUNKYLDQDVNIKVIQGPAAIRLPSPDVKYKSYNEG 421

Qy 423 IVRNUSCRKEDQCHPKPVLPPDLPBLKLYKAKNVRIDKHYLFDQW-LAVRSNSNTNGGG 481
 Db 422 IARNISCREPQNQHFKPVLKFLPKRLHAKSDRLEPFLTYDQFWQQLLNPSRKYCSG 481

Qy 482 NHGYNNEFRSMEAFLAHPSPKETTEAPPENIEVNMCDLIRIQAQDNGTHGLNLH 541
 Db 482 FHGSNDPSNMQDMLPQHGFGEKIAETTENEVNMCDLNLTAAPNNOTHGSNLH 541

Qy 542 LLKVBYFEPYKPSVHAEVSKFVCGFANPLPESLDFC-PHQNSTQLEVNQMINLTOEBI 600
 Db 542 LLKNPVTYPTKPKVHPLVQCPFTN-PRDNLGSCSNPSI--LPIEDFOTQENLTYABE 597

Qy 601 TATVKVNLPGCRPRVYQKTYDQHCLLYHREYVSGFGKAMEMPMWSSYTPQBLGPTSPLPPT 660

Qy 598 KLIKHETPLPGPRVYQKTYDQHCLLYHREYVSGFGKAMEMPMWSSYTPQBLGPTSPLPPT 655

Qy 661 VPDCLRADYVPPSESOQCSFYLADKNTHTGFLYPPASNRTSQYDQIMPLNTSYTDR--NDSFSTD 719

Qy 656 FSNCIYQDFRFLPSVHKCSFYQNTKVSYGFLSPQNLKNSGTYSEALLTNIVPMQ 715

Qy 720 EFRKWDYFESVLLKHAERNGYNVSGPFLDYNQDGHFADPDEITHK---LANTDVP 776

Qy 716 SFQV1WRYFHDTLRKYAERNGYNVSGFVDFDGRCDSLNLRQRRVVERFTHI 775

Qy 777 PTHFFVVLTSKNSKSHTPENCPGMLDLPPLIPHRPTNVECPGKPEALWVERFTHI 836

Qy 776 PTHFFVVLTSKNSKSHTPENCPGMLDLPPLIPHRPTNVECPGKPEALWVERFTHI 834

Qy 837 ARVRDVEELLSTGDFYDQKVOVSEBILQKLYLPTF 871

Qy 835 ARITDVEHITLSSFQQRKEPVSDILKLTALHPTF 869

RESULT 4
 US-09-392-946-1
 ; Sequence 1, Application US/08392946
 ; Patent No. 5939269
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / APPLICANT: The Regents of the University of California
 / APPLICANT: Goldfine, Ira D.
 / APPLICANT: Gruppe, Andrew
 / APPLICANT: Maddux, Betty A.
 / APPLICANT: Stewart, Steven
 / APPLICANT: Timothy A.
 / TITLE OF INVENTION: Antagonists to Insulin Receptor Tyrosine
 / NUMBER OF SEQUENCES: 1
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 1 DNA Way
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS DOS
 / SOFTWARE: Winpatin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/392,946
 / FILING DATE:
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/182241
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / FILING DATE: 14-JAN-1994
 / REGISTRATION NUMBER: 36,575
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650/245-8228
 / TELEFAX: 650/952-9881
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 925 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 / US-08-392-946-1

Query Match 52.0%; Score 2498.5; DB 2; Length 925;
 Best Local Similarity 53.1%; Pred. No. 8.8e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EOPVKK---NTLK---KYKACIVLALLVIMSTGGLGIGLQLRKLEQGSCCRKCFDAS 62
 Db 57 EEPLEKXARARTAKDPTNLYKVLSSVCLTILGICF1GKPKSAKEVSKGRCFERT 116

Qy 63 FRGLENCRDVAOKRGDCCDWDFDTCVESTRIMCNKFRGETEELASLGSCSDDCLK 122
 Db 117 F---GNCRDAAVCLGNCCLDQTCIEPHIWTNCNKFRCGEKRLTRSLCAGSDCKDK 173

Qy 123 KDCCADYKSVCOGETSWLEENCDAQOQSCCPGFDLPPVILFMDGPRAEYLTTWDTLMP 182
 Db 174 GDCDINTSSVCOGEKSVEEPEINEPQCPAGFEPPTLISLDFRAEYLHTNGGLP 233

Qy 183 NINKLKTGIGHSKMMRAMPKTFPKNHHTVLTGYPESHGIDDNMMYDNLNKNFESLSK 242
 Db 234 VTSKLKCCGTYTMNMRVYPTPTEPHNSYITGLYTESHGIDDNMMYDNLNKNFESLSK 293

Qy 243 EQNPAWNGQPKWLTAMQOGLRATYTFPQGSEVAINSSFPSPYMPNGSVFPEERISTL 302
 Db 294 EKPNPENYKGEPIWVTAKYGKSGIFFWPGSDVLENGIFDIDYQNGSVFPEERILAV 353

Qy 303 LKWLDPKAERPRFETYMFEEPDSSGHAGGPVSAVIRAKQVVDHAFRMGLKGRLKORNHL 362

RESULT 5
 US-08-504-169-1
 Sequence 1, Application US/08504169
 Ent. No. 5968508
 GENERAL INFORMATION
 APPLICANT: Goldfine, Ira
 APPLICANT: Grupe, Andrew
 APPLICANT: Henzel, William
 APPLICANT: Maddox, Betty
 APPLICANT: Spencer, Steven
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Harrison, Denise M.
 TITLE OF INVENTION: Antibodies to Insulin Receptor Tyrosine Kinase Activation Inhi
 NUMBER OF SEQUENCES: 1
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.5 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/504,169
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14893
 FILING DATE: 28-Dec-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/182241
 FILING DATE: 14-Jan-1995
 ATTORNEY AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0875P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 925 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-504-169-1

Query Match Score 2498.5; DB 2; Length 925;
 Best Local Similarity 53.1%; Pred. No. 8.8e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EQPVK---NTLK---KXIAICIVLALLIVINSGLGLGLKLEKQSGCRKCFDAS 62
 Db 57 EPLERKAAPARTADPNTYKVLISLIVSIVCLITLGLCPGLKDSCAEVKSCGRCERT 116
 Qy 63 FRGLENCRCRDVACKDGDCCWDPEPDTCVESTRIMCNRFRGCTERTRASLCSDDCQLQK 122
 Db 117 P---GNCRCDACTYELGNCLDQBTCEPEHIVTNKFRGCKRLRTRLSCACSDDKDK 173
 Qy 123 KDCCADYKSYCVOQEGTSWLFCENCQTAQSOCPGFDLJPPVILPSMDGFRAEYLTYDQJLMP 182
 Db 174 GDCCINYSSVCQGBEWSWEPBCEBNEBOPCPAFETPTLFLDGRAEYHTWGDLLP 233
 Qy 183 NINKLKTGITHSKYKMRAMYPTKTFPNNPHYTITCGLYPSHSGIDDNMMYDVNLKNFSSSSK 242
 Db 234 VISTKLKKGCGTQNMPPYPTKTFPNNPHYTITCGLYPSHSGIDDNMMYDVNLKNFSSSSK 293
 Qy 243 EONNPAAWHEGQPWMLTAMYQGLKAATYFWPGSEVAINSSFPSTYMPNGSVPPEERSTL 302
 Db 294 EKFENPEWYKGPB1WVTAKYQGLKSGTF1FWPGSDVEINGIFPDYKMMNGSVFEERLAV 353
 Qy 303 LKWLQLPDRBPHFTYIILEPPISSGHSYGPSSSEVKAHQVTDHAFGMLMEGLKORNHL 362
 Db 354 LQWLQLPDRBPHFTYIILEPPISSGHSYGPSSSEVKAHQVTDHAFGMLMEGLKORNHL 413
 Qy 363 NCVNILLIADHGMDQTYCNKMEYNTDYEPRINFFYMEGAPRIRAHNIIPHDDFSNSEE 422
 Db 414 RCLNLILISDHGMEQGSKCKYIVIANKYLGUDVNKIVYDQVNLNTQOEI 473
 Qy 423 IVRNLSCKRKPDQHFKPVLTPDLPKRLHYAKNVRIDKYLHFDQWQ-LAVRSKSNTNCGGG 481
 Db 474 IARLJSCHREPQHFKPVLQHFLRHLAKSDRIEPTFYLBDQWQALNPBKRYCGSG 533
 Qy 482 NHGYNNEPESMEAIFLAHGSPSEKETVPEPENIEVNLMCDLRLICAPNGTHSINH 541
 Db 534 FRGSDNIVSINMQFLFGPFGHGIADTFNTEVYNLMCDLNLNTAPANGTHSINH 593
 Qy 542 LLXTPFYPERSHAREDSKSVGPNTQPTESLDCCF-PHLNQNSTOLEQVNQMLNLTQEII 600
 Db 594 LLXNPVYTFKHPKEVPLVQCPTRN-PRDNLGCSCPSTI--LPFEDFOTQFNLTVAAE 649
 Qy 601 TATVKNLDFGRPRVQXNVDHLLYREYVFGKAMRMPWSSTVPOQJGDTSPBPPT 660
 Db 650 KLIKHETLPYGRPRVQXNVDHLLYREYVFGKAMRMPWSSTVPOQJGDTSPBPPT 676
 Qy 661 VPDCLRADYRVPESSESQCSFYLADKQHLYGFLYPPSNRTSDQY-DALITSNLYPMYE 719
 Db 708 FSNLYQDFRIPUSPVKCSFKNNTKVSIGLSPPLNKNSSGIVSEALLTNNVPMYQ 767
 Qy 720 EFRKMDYFHSVLLIKHATERNGVNVSQGPFDYNYDGHFADPDEYTKH--LANTDVP1 776
 Db 768 SFQVWRYFHDTLRKYAEERGNVNVSQPVFDDYDGRCDSENLRQKRRVIRNOEILI 886

Qy 777 PTHFIVLTSKCKNSHTPNCPCGWLDPVLTPIHPRPTVNECPEGKEALAYBERTAHI 836
 Db 828 PTHFIVLTSKCKNSHTPNCPCGWLDPVLTPIHPRPTVNECPEGKEALAYBERTAHI 886

Qy 837 ARVDVELLTGLDFYQDKYQVPSSEILQKTYLPTF 871
 Db 887 ARITDVEHHTGGLSFYQQRKEPVSDILKLTKLHLPFT 921

Qy 900 NUMBER OF SEQUENCES: 1
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.5 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/504,169
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14893
 FILING DATE: 28-Dec-1994

Qy 354 RCLNLILISDHGMEQGSKCKYIVIANKYLGUDVNKIVYDQVNLNTQOEI 600
 Qy 363 NCVNILLIADHGMDQTYCNKMEYNTDYEPRINFFYMEGAPRIRAHNIIPHDDFSNSEE 422
 Qy 3720 EFRKMDYFHSVLLIKHATERNGVNVSQGPFDYNYDGHFADPDEYTKH--LANTDVP1 776
 Qy 3768 SFQVWRYFHDTLRKYAEERGNVNVSQPVFDDYDGRCDSENLRQKRRVIRNOEILI 886

Qy 777 PTHYFVYLTSCKNSHTPENCPGNLDVLPLFIIPIHPTNVESCPCKPBAALVVEERTAHI 836
 Db 828 PTHFETVLLTSCKDTSQTPLHCEN-LDTIAFLPHTDSEISVGHKHDSSVNEELLMLHR 886

Qy 837 ARVDFVLLTGLDFYQDKYQVPSSEI-LQKTYLPTF 871
 Db 887 ARITDVEHTGTSYQQRKEPVPSDILKTKLTHLPTF 921

RESULT 6
 PCT-US94-14893-1
 / Sequence 1, Application PC/TUS9414893
 / GENERAL INFORMATION:
 / APPLICANT: Genentech, Inc.
 / The Regents of the University of California
 / Goldfine, Ira D.
 / APPLICANT: Grube, Andrew
 / APPLICANT: Maddux, Betty A.
 / APPLICANT: Spencer, Steven
 / APPLICANT: Stewart, Timothy A.
 / TITLE OF INVENTION: Antagonists to Insulin Receptor Tyrosine Kinase Inhibitor
 / NUMBER OF SEQUENCES: 1
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 460 Point San Bruno Blvd
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/TUS94/14893
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/182241
 / FILING DATE: 14-JAN-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Kubinec, Jeffrey S.
 / REGISTRATION NUMBER: 36,575
 / REFERENCE/DOCKET NUMBER: 875P1PCT
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/952-9881
 / FAX: 910/371-7168
 / INFORMATION FOR SEQ ID NO:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 925 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / PCT-US94-14893-1

Query Match 52.0%; Score 2498.5; DB 5; Length 925;
 Best Local Similarity 53.1%; Pred. No. 8.8e-235;
 Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;

Qy 10 EQPVKK---NTLK---KYKIACTIVLALIVIVMSLGLGLGLRKLEQKSCRKCFDAS 62
 Db 57 EEPLEQKARATAKDNTPYKVLNLSVCLVLTIGCFGLKESCAKEVKSCRKCFERT 116

Qy 63 FRGLENLRCRDYACKORGDCWDFFDTCVBSTRIMCNKPERCGETTRLESLCSCDCQK 122
 Db 117 F---GRCRCDACVGLNCCLDQTCIEPEHHTCNKPERCGERKRLTSLCSCDDDKDK 173

Qy 123 KDCGADYKSVQGETSMLENCDTAQSQCPEGFDLPPVILFSDMDGTAEMLYTWDLMP 182
 Db 174 GDCCCLINNSVSVQGEKSWVEEPCES-NEPOCPAGETPPTPLFLSDGFFAEYLHTWGGLP 233

Qy 183 NTNKLKTCGIGHSKMYRAMYPTKTFPHNHTIVGLYBESHTGIDNMMYDYNLKNKNSLSSK 242
 Db 234 VSKLKGCGTGYTAKMRPVYPTKTFPHNHTIVGLYFESHTGIDNMMYDPKNNASLNSK 293

Qy 243 EQNPAPWPHGOPWLMYTAMYQGKKAAYTFWPESEVANLNGPSITINPYPNGSVPFERRISTL 302
 Db 294 EKPNPBNWKGEPIWTAKYQGJKSGF-FWPSSDVETNGIFIDYKNGSVPFERRILAV 353

Qy 303 LKNDLPAERPRFYTMYPEBDSSHAGGGSYASARTIKALQVYDHAFCGMLMEGIKQRVNLH 362
 Db 354 LQWQLQPLDERRPFTYLEDSSHAGGGSYVVISSETIKALQRVDGKVMMDGKRLBNLH 413

Qy 363 NCVNILLIADHGMDOQTYCNKMEYMTDYPRTNFYMEGAPRIRAHNIPHDEFFSNSEE 422
 Db 414 RCINNLILSDHGMEQGSCKKTYLNCYLGDKRNKTYIYGPAULRPSDVDKYFNYEG 473

Qy 423 IVRNLSCKRDPDQKRPVLTPLKPLKRYAKRVLKDHLEFDQW-LAVBSKSNTCNGGG 481
 Db 474 IARNLSCREPNOFKPVTPLKHFPLKRFHAKSDRIELTFLPDWQQLANPNSERXCGSG 533

Qy 482 NHGYNNEFRSMEIAFLAHGPSKKEKTEVEPSENIEYNLMDLIRIOPAQNNGTHGSLNH 541
 Db 534 FHGSDDVYNSNMQALFVYGPGRKHGEADTENIETYNLACDLANITPAPNGTHGSLNH 593

Qy 542 LLRVPFYEPSHAEVSKFSVCCPFSKYLADKNTIHPYDPAQNSRNTSDQY-DALITSNLVPMYE 600
 Db 594 LLKNPVPYTPKHPKEVHPLVQCFPTRN-PRDNGSCNPSTI--LPEDFQTNLUTVAEE 649

Qy 601 TATVKVNLPFGGRPVLQKRNVDHLLYTHEYYSGFKAMRMPWSSYTPQOGDTSPPLPT 660
 Db 650 KIKKHEPYPGRPVLKQENTICLSSOQFNSGQDILMPLWTSYTVDR--NDSFSTED 707

Qy 661 VPDCGRADYRVPPSESKCSFYLADKNTIHPYDPAQNSRNTSDQY-DALITSNLVPMYE 719
 Db 708 FSNCIYQDDEPILSPVHKCSFYKANTRVSYGLSPQLNKNSGIVSEALITNIVPMQ 767

Qy 720 EFRKMDYFHSVLLKHTERNGVNTVSGPFLDNYDGHFDPDDETKH--LANTDVPI 776
 Db 768 SFQVITWRYFHDTLURKFAEERGVNTVSGPFLDGRCSLNRNQKRRVIRNQEBILI 827

Qy 777 PTHYFVYLTSCKNSHTPENCPGWJLWLPFTIPHRTNVRSCEPECKPEALWEEERTAHI 836
 Db 828 PTHFIVTWSCKDTSQPLRCN-LD7JAF1PHRFDNSESCVRGHDSSWEEULLMLHR 886

Qy 837 ARVDFVLLTGLDFYQDKVQPVSEIQLQKTYLPTF 871
 Db 887 ARTDVEHTGTSYQQRKEPVSDILKTKLTHLPTF 921

RESULT 7
 US-09-438-906-4
 / Sequence 4, Application US/09438906
 / Patent No. 6465185
 / GENERAL INFORMATION:
 / APPLICANT: Goldfine, Ira
 / APPLICANT: Trischitta, Vincenzo
 / APPLICANT: Pizzati, Antonio
 / APPLICANT: Vigneri, Riccardo
 / APPLICANT: Frittitta, Lucia
 / TITLE OF INVENTION: Polymorphic Human PC-1 Sequences
 / FILE REFERENCE: 9076-089
 / CURRENT APPLICATION NUMBER: US/09/438,906
 / CURRENT FILING DATE: 1999-11-18
 / PRIOR APPLICATION NUMBER: 60/108,853
 / PRIOR FILING DATE: 1998-11-18
 / NUMBER OF SEQ ID NOS: 35
 / SEQ ID NO 4
 / LENGTH: 873
 / TYPE: PRT
 / ORGANISM: H. sapiens
 / US-09-438-906-4

every Match	51.9%	Score	2494.5	DB	4	Length	873
est Local Similarity	53.0%	Pred. No.	2e-234				
atches 464; Conservative	138; Mismatches 250;	Indices	23;	Gaps	11;		
10 EOPVKK --- NTLK -- KYKACIYVLLALIVMSIGLIGLGLRKLEKOGSCERKCFPDS	62						
5 EEEPLEKAARATAKIDNTYKVLSTLVSVCVLTTLGCTGLKPSCAKEVKTSCKGRCPERT	64						
63 FRGLIENCRDVAACKRGDCWDFFDTCTCVESTRINCNKPERCGETRLEASLCSGDCDCLKQ	122						
65 F --- GNCRDAACVNEIGNCCUDYQSTCIEBEHINTCNKPERCGERLTSCLACSDCKDQ	121						
123 KDCDAAKSVQCGEITSWLENCDTAQSCQPEGLPPVTLFSDGFAEYLTTWDTEMP	182						
122 GDCCTNYSVQCGEESWWEPCESENQCPGAEPTPTTTLFSDGFAEYLHTWGGLP	181						
183 NINKLKGIGTHSKYKRAMPTKTFKPNHYTIVTGLYPESHGIDDNMYDNVNLKNSLSSK	242						
182 VSKLKKCGYTKNPKPVYTKTFRNHYSTVGTGLYPESSGIIIDNKMPKNDASPLSK	241						
243 EQQNPAWNGWEGSPGMMLTAMYQCLKAATYFWGSEVYLINGSFPSTYMPYNGSVPPFEERISTL	302						
242 EKPNPEWYKGPEPIWNTAKYQCLKSTTFWFNGSDVTEINGFPDLYKMMNGSVPPFEERILAV	301						
303 LKWLIDPKAERPRFVTMYFEEPDSSGCHAGGPVSARVIRALQVYDHAFGMLMEGLKORNHL	362						
302 LQWLQPKDERPHFTYLYLEEDPSSGHSYGPVSSSVIRALQVYDGVNMLGJKEUNLNH	361						
363 NCVNLT1LADHGMDQTYCNKMEYNTDYFPRINFFMYEGPAPTRAHNIPHDFFSENSE	422						
362 RCLNL1LISDGMEQSCSKRYIYLNKLGDQVNRKVIYQPAARLPSDVPDKYKSYFNEG	421						
423 IVRNLSCKRPDKHFKYLPDPLKHLHYAKNVRIDKTHLYFDQW --LAVRSKSNTNCGGG	481						
422 TARNLSCREPQHFKYLPDPLKHLFAKSDRLEPLTYLDPEWQALNPSRKYKCGSG	481						
482 NHGYNNEFRSMEAI1FLAHGSPKEKTEVEPPRENTEVNNLMDLRLIQAPANGTHGSLNH	541						
482 FHGSIVNEFSNQALFVGYGRGPKHSTEADTFENTEVNNLMDLNLTPAPNNTHGSLNH	541						
542 LIKVPYEPSHAEEYSKESKGFMPLTESLDCFC - PHLNQNSTQLEQVNQMLNLTQEEL	600						
542 LIKNPVYTPKHPKVEVPLVQCPFTN - PRDLNGCSNPSEI --- LP1EDFOTNLTYAE	597						
601 TATVKVNLPGRPRYLQKNDHCLJLYRETVSGKGKAHRMPWISSYTPQLGDTSPPLPT	660						
598 KLIKHKTLPGSPRVLQKENTICLISQHQMFSGQYSDQILMPLWTSYVYD - NDSEFSTD	655						
661 VPDC1RADVRVPPSSQKCSPLYLAQKNTHTGFLYPPASNRTSDSQY - DALITSNLVMYE	719						
656 FSNCLYQDFRPLSPVHKCSFYKNTKVSQPKVSPQLNKNSGIIYSEALLTINIVMYQ	715						
720 BFRKMDYFHVVLLKHAFTERGNGVNVSGPFDYNDGHFADDEITH -- LANTDVP1	776						
716 SFQVITWRYFHDTLLRKYAEERNGVNVSGPVEFDYGRCDLSLENLQKRRVIRNQEILI	775						
777 PTHFVLTSCKDTSOTPLHCEN-LDTLAFILPRTDNESECVHGGHDSSWTEELLMLHR	834						
837 ARVRDVEYLTSGLDFYQDKYQPVSEBLQLKTYLPFF	871						
925 PTHFVLTSCKDTSOTPLHCEN-LDTLAFILPRTDNESECVHGGHDSSWTEELLMLHR	836						
776 PTHFVLTSCKDTSOTPLHCEN-LDTLAFILPRTDNESECVHGGHDSSWTEELLMLHR	834						

RESULT 8
US-08-346-455B-69
; Sequence 69, Application US/08346455B
; Patent No. 5711167
; GENERAL INFORMATION:
; APPLICANT: UNITED STATES OF AMERICA
; APPLICANT: OF HEALTH AND HUMAN SERV
; APPLICANT: OF HOMELAND SECURITY, COMMER
; APPLICANT: ON TRANSPORTATION, SECUR

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (121) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
STRAND: 1
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-69

Query 304 KWLDLPAERPRPYTMYFEEDSSGHAGPVA----- 336
Subject 291 RWTLPDHERSVAFYSEQPDPSCHSKYQPFGEPESSYGSPTPAKRKRKVAPKRKRQER 350

Query 337 -----RVTALQVVDPLKQKLRLRCVNTVIFG 410
Subject 351 PVAPPKRRKRKTHDHYAETRDKMTNPREDKIVQMDGLKQKLRLRCVNTVIFG 410

Query 372 DHGMDOTYCNRMEYMTDYFRINFFYMEGPAPIR-----AHNIPHDFSFNSBETIVRNLS 428
Subject 411 DHGMDVTCDETEFLSNLTNVDDITLIVGTLGIRKSFESNNAKYD-----PKAIIANLT 465

Query 429 CRKPDHFKPYLTDPLPKRLHYAKNVRDVKHLYFDQOW-----LAVRSKSNNTNC-GGG 481
Subject 466 CKKPDHFKPYLQKLQKLPKRLHYANTRRIDIHLIVRWHVARKPLDLYKPKSGKCFQG 525

Query 482 NHGYNNEFRSMEAIFLAGHPSFKERKTEVFFENTEVYIMCDLRLICPAHNGTGSLNH 541
Subject 526 DGFDFDKRVSNSQTQVPGGTFKXKIVPKFENELVYNCNDLGLKKEAPNGTGSLNH 585

Query 542 LLKVPFYEPSHAEFSKSFVCGFANPLPESLDCFC-PHLONSTOLESYQNONMLNQBEI 600
Subject 586 LLRTNTFRPTMPEEVTRPNPGIMYQSDFDLGTCDRVEPKNKLDDLNKRLHTK---- 641

Query 601 TATVKVNLPLPGRPRVLIQPKVNDHCLLYREXVSGFKKARMKPMWSYTYVQGLDTSPLPPT 660
Subject 642 GSTEEERHLLGPRATYR-TRYDLYHTFESGYSEIILMLWLTTSYTSKQAEVSSVPDH 700

Query 661 VPDCLERADVRVPPSESQKCSFYLADKINRHFGLYPPASARTSDQYDNLITSLVPMYEE 720
Subject 701 LTSCVRPDVRSVPSFSQLCLAYKNDKQMSYGLFPPVYSSPEAKYDPLVNTNMVPMYPA 760

Query 721 FRKWDYFHVSULLKTAERANGVAVSGPLFDNYDGHFDAPPBTKHLANTDVPFPTY 780
Subject 761 FRKVNKFQRLVCKYASERNGVAVISG2FDYDGDGLHDETEKIKQYVEGSSIPVPTY 820

Query 781 FVVLTSCKNSHTPENCPGMVDFLIFIPIRPTVNESECEGRBALWVTEERTAHARV 840
Subject 821 YSITTSOLDFQPADKCDGFLSVSSRFLPHRDNECSNSSEDESKWTEELMKMHTARV 880

Query 841 DVELITGLDFYQDKYQVPSBILQKTYLPIFETI 875
Subject 881 DHEHLLSDFFRKTSRSPBILITLTYLHYESI 915

RESULT 9
US-08-977-221-69
Sequence 69, Application US/08977221
Parent No. 5084059

GENERAL INFORMATION:
APPLICANT: UNITED STATES OF AMERICA; DEPT.
TITLE OF INVENTION: OF HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: MOTILITY STIMULATING
TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: U.S.A.
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,221
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,455
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,182
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/822,043
FILING DATE: 17-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 2026-4149US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (121) 751-6849
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 915
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: No
FEATURE:
NAME/KEY: A2058 ATX protein
LOCATION:
STRAND: 1
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-977-221-69

Query 722 QNPNPWNHGQPMWLTAMYQGLKATYFPGSEVAIINGSFPSYMPYNGSVPFEERSTILL 303
Subject 723 KENHRWGGQPLWITATQGVQKATPFM-----SVVIPH-----ERRUTIL 290

Query 744 INKLTKGHSKVNRAKMPKTKFPPNHTITVCLYPPBHGIDDNAMDVLNKNSLSSKE 243
Subject 745 DCCADYKSYQGGETSWLENCNTDAQKQSCPPEGFDLPPVILSMDGPRAEKLYTWDLMPN 183
Subject 746 RGLENCRDVAQKDRGDCWDFDTCYESTRIMCNKFRGCTERTRLEASLSCSDPQOKK 123
Subject 747 AGPPPCRDNKLCKSYTSCHDFBUELKATRGWECYDRCGEVRVNEACHCSEDCLARG 128

Query 748 24 ACTIVALLVYMSIGLGLGLRKLEK-----QGSCRKKCFCDAF 63
Subject 749 SCQISLFFAVGSISICGFTAFRRIKEAGWEGPPVILSDEPWTNTSGSKGRCEBLOE 68
Subject 750 DCCCNVQVCKGSHWDDCBEIKAECPAFVPRPLIITFVGDGRASYSMKGSKVMNP 188

Query 751 INKLTKGHSKVNRAKMPKTKFPPNHTITVCLYPPBHGIDDNAMDVLNKNSLSSKE 243
Subject 752 DCCADYKSYQGGETSWLENCNTDAQKQSCPPEGFDLPPVILSMDGPRAEKLYTWDLMPN 183
Subject 753 184 INKLTKGHSKVNRAKMPKTKFPPNHTITVCLYPPBHGIDDNAMDVLNKNSLSSKE 243
Subject 754 189 IEXKPSGCHSHPSYMPVYPTKKEPPLVYLTATQGVQKATPFM-----SVVIPH-----ERRUTIL 290

Query 755 124 DCCADYKSYQGGETSWLENCNTDAQKQSCPPEGFDLPPVILSMDGPRAEKLYTWDLMPN 183
Subject 756 129 DCCCNVQVCKGSHWDDCBEIKAECPAFVPRPLIITFVGDGRASYSMKGSKVMNP 188

Query 757 184 INKLTKGHSKVNRAKMPKTKFPPNHTITVCLYPPBHGIDDNAMDVLNKNSLSSKE 243
Subject 758 189 IEXKPSGCHSHPSYMPVYPTKKEPPLVYLTATQGVQKATPFM-----SVVIPH-----ERRUTIL 290

Query 759 304 KWLDLPAERPRPYTMYFEEPDSSCHACGPVA----- 336
Subject 760 304 KWLDLPAERPRPYTMYFEEPDSSCHACGPVA----- 336

Query 761 291 RWLTPDHERPSVTAFYSEQDPSGHKXGPPFSESSYGSPTTPKRVAPKRQER 350
Subject 762 291 RWLTPDHERPSVTAFYSEQDPSGHKXGPPFSESSYGSPTTPKRVAPKRQER 350

Query 763 351 PVAPPKRRKRKTHDHYAETRDKMTNPREDKIVQMDGLKQKLRLRCVNTVIFG 410
Subject 764 352 DGHMDOTYCNRMEYMTDYFPRINFFYMEGPAPIR-----AHNIPHDFSFNSSEEIVRNLS 428
Subject 765 411 DGHMDVTCDRTEFLSNLTNVDDITLPGTIGRIRSKFSNNAKVD-----LAVRSKSNNTNC-GGG 481

Query 766 429 CRKPDQHFKPYLTDPLPKRLHYAKNVRDVKHLYFDQOW-----LAVRSKSNNTNC-GGG 481
Subject 767 466 CKKPDQHFKPYLQKLQKLPKRLHYANTRRIDIHLIVRWHVARKPLDLYKPKSGKCFQG 525

Query 768 482 NGYNNEFRSMEAIFLAGHPSFKETKEVFPENIEVNLMDLLRQAPANNGTHSLNH 541
Subject 769 482 NGYNNEFRSMEAIFLAGHPSFKETKEVFPENIEVNLMDLLRQAPANNGTHSLNH 541

RESULT 10
 US-09-483-831B-69
 Sequence 69, Application US/09483831B
 Patent No. 6117338
 GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY
 APPLICANT: SCHIFFMANN, LANCE
 APPLICANT: KRUTZCH, HENRY
 APPLICANT: MURATA, JUN
 TITLE OF INVENTION: AUTOTOXIN: MOTILITY STIMULATING PROTEIN USEFUL IN
 TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
 FILE REFERENCE: 2026-4149054
 CURRENT APPLICATION NUMBER: US/09/483, 831B
 CURRENT FILING DATE: 2000-01-17
 PRIOR APPLICATION NUMBER: 07/892, 043
 PRIOR FILING DATE: 1992-01-17
 PRIOR APPLICATION NUMBER: 08/249, 182
 PRIOR FILING DATE: 1994-05-25
 PRIOR APPLICATION NUMBER: 08/346, 455
 PRIOR FILING DATE: 1994-11-28
 PRIOR APPLICATION NUMBER: 08/977, 221
 PRIOR FILING DATE: 1997-11-24
 NUMBER OF SEQ ID NOS: 70
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 69
 LENGTH: 915
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 FEATURE:
 OTHER INFORMATION: Polypeptide
 US-09-483-831B-69

124 DCCADYKSVCGETSWILEENCDTAQOSQCPEGFDLPPVILESMQGFRAEVLYMTDTLMPN 183
 129 DCCTNYQVYCKGESEHWTDDCEBEIAECPAGFVRPLIFSVQDFRASYMGSKGSKVMEN 188
 184 INLKTCIHSKYMRAKPTKCFPNEYTTIVGLEYSESGTIDNNYDVALKNSFLSLSKE 243
 189 TEKURSGTHSPMRYPTKCFPNULYTATGLYEPHSHGIVGNSMYDPVDFHLSRRE 248
 244 QNNPAWEGQPMWLTANQGKAAATFWPGSEVAINGSPPSIYMFYNGSVPFEERISTTL 303
 249 KENHRWMGQPLWITAKQGVKAGTfW ----- SVVPH-----ERRLTL 290
 304 KWLDLPAERPRPYTMFEEDPSGCHAGGPVSA----- 336
 291 RWTLPDHERPSVYAFSEQPDSFGHKYGPGESESSYGSPPFTAKPKRKVAPKRRQER 350
 337 -----RVTKAQVQDHFAGMIGKJQRNLHNCYNTIILIA 371
 351 PVAPPKGRRKTHRDHYAETRQDKTNPREIKVGJMDGKJQLKLRCCVNVFG 410
 372 DHEMDQTYCNCNEYMTDFPRINFFYMEGAPRIR-----AHNTPHDFESFNSEBIVRNLS 428
 411 DHEMEDTCDRTEFLSFLTNDDITLVPGTGLGR-TSKFSNNAYD-----PRAJALD 465
 429 CRKPDPDKPKPVLTPDPLKRLHYAKNVRDVKHFLVDQON-----LAVRSKSNTNC-GGG 481
 466 CRKPDPDKPKPVLTKHFLVRLRVRHVARPKLDPKSKCFRKG 525
 482 NAYYANERPSMAMELIHCPSPKETEVFENIYVNCMDLRLRQAPANGTHGSLNH 541
 526 DHEFDNCNSMOTVFGYGPFTKVKPFFENTLYNCMDLGLKPAPNNGTHGSGNH 585
 542 LKVKPFTEPSHAEVSKPSVCGFANPLPTSLDCEC-PHQLNSTOLQVQNMUNLTQBEI 600
 586 LIRTNTTRPTMEEVTRPNPGIMYLOSDDELGCTCDPKVNLKRNKHTK----- 641
 601 TATVKVNLPGPRLQVQDHLLYREVSGFGKAMRMPPMSSTYVQLGDTSPPLPT 660
 642 GSFEERHILYGPAPLXR-TRYDLYHTDESGYESEIEMLWTSYTSKQAEVSYDH 700
 661 VPDGLRADVRYPSSESCSCKSTYLAQKNTTGFPLYPAHRTSDSQYDALTTSNIVPMYEE 720
 701 LISCVRDPDVPSFSQNCAYKNDKQMSGFLFPYSSPEAKYDAPLVTNMPMPA 760
 721 FRKWDYKPHSVLILKHTATERGVNVVSQFIDYNDGHFADPELTKHANTDVPPIPHY 780
 761 FKVWNFTQRLVKKCALSERNGVNVNTSGPFDYDGLHDTEDKIQTYEGSSIPVPHY 820
 781 FVVLTKPSKNSHTPENGPWNLVLPPTIPIRPTNTVSCPEGKPPALWVEERFTAIIARVR 840
 821 YSITSCUDFTOPADICDGPVSSFLPRPDNECSNSSEDESKWVEELMKNHTARVR 880
 841 DVELITSLDFQDKVQFVSETEILKTKYLPFETTI 875
 881 DIBHLSLDFPRKTSRSRSTYPEILTKYLYTSEI 915

RESULT 11
 PCT-US95-06613-69
 Sequence 69, Application PC/TUS9506613
 GENERAL INFORMATION:
 APPLICANT: STRACKE, MARY; LICHTA, LANCE;
 APPLICANT: SCHIFFMANN, ELLIOTT; KRUTZCH,
 APPLICANT: HENRY; MURATA, JUN
 TITLE OF INVENTION: MOTILITY STIMULATING
 TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS: 69
 ADDRESS: MORGAN & FINNEGAN
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK

COUNTRY: U.S.A.
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/06613
 FILING DATE: 24-MAY-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/346,455
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/249,182
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/822,043
 FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36,434
 REFERENCE DOCKET NUMBER: 2026-4149US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 755-4400
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 915
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: No
 FEATURE:
 NAME/KEY: A2058 ATX protein
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PCT-US95/06613-69

Query Match 42.5%; Score 2040.5%; DB 5; Length 915;
 Best Local Similarity 40.5%; Pred. No. 5.2e-190;
 Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

QY 24 ACIVLLALVNSLGLIGLGLRKLEK-
 Db 9 SCOTISLFTFAGVSYICIGFTAAKRAEGWEGPPTVLSQVPSLQLQTYLPFTETI 875
 QY 124 DCCADYRSVCOGETSWLLENCDTAQQQCPGQFDLPPVILEMSDGFRAEYLWTMDLMPN 183
 Db 129 DCCTNYQVVKCGEBSHWYDDCCEIKAECPAGEYRPLIFSVDCGFRASMYKGSKVN 188
 QY 64 RGLENCRDVAKKDQGCCWDPDTCVESTRIWMCNKFRGETRLEASLSCSDDCQK 123
 Db 69 AGPPDCREDNLCKSYTSCCHDDELCKTARGWECIKDRGEVANBACHCSBDCLARG 128
 QY 244 QNNPAWHQOPWHLTAQYQGLKATATWPGSEVAINGSFPSIYMPNGSVPFEERISTIL 303
 Db 249 KFNFRWKGQPLWTAQXQVAGTFTW-----SVVPH-----ERRIL 290
 QY 304 KMLDLPKAERPRPYTMFEEPDSSGHHGPVSA----- 336
 Db 291 RWLTPDHERPSYAFSBQDPSGHXGPPEESESGSFTPAKPKVAPRREER 350
 QY 337 ----- 371
 Db 351 PVAPPKERRKTHRDHYAETRQDKTNPLREIDXVGQLMGKLQLKLRCRNVIVFG 410

QY 372 DGHMDOTYCNRMBYWMTDYPRINFFYMEGPAPIR--AINTPHDFSENEEIVRNLS 428
 Db 411 DGHMEDVTCDRTEFLSNYLTVNDDITLVPGLTRGKPSNNAKYD----PKAIIANLT 465
 QY 429 CRKPODHFKEYLTPLPKSLHYAKNRIDKVKHFLVDQW-----LAVRSNTINC-GGG 481
 Db 466 CKKPOQHFKPLQKHLPLRKHANNRVEDHILVERWHARKPLDVKKPSGCKFFQG 525
 QY 482 NHGYNFRFREMEAFLAQRGSPSFKEKTEVFPFENIYVNLMDLRLQAPANGTHGSLLNH 541
 Db 526 DHGFKNQVMSQMTVYVGPTFKTPFENIYVNLMDLGLQAPANGTHGSLLNH 585
 QY 542 LLKVPFYEPPSHAEVSKFESVCGFANPLTESLDFCFC-PHLONSTOLBQVNOMNLNQBEI 600
 Db 586 LLRNTFRPMPMEETRPNPGMLQSDFDLCTDDKVEPKNKLDBLNKLHTK---- 641
 QY 601 PATVWNLPLFGRPRWPLQKNUYDHCLLYHSEYVSGFGKAMRMPKWSSTYVPGDTSPLPPT 660
 Db 642 GSTERHLLYGRPAVLRY-TRYDLYHDFESESYEFLMLWTSVSKQEVSSYVPDH 700
 QY 661 VPDCRADYRVPSSEROKCSFYLADKNITHGELYPASNRNTSDSOYDALITSNLVPMYEE 720
 Db 701 LRSCTRDPYRVPSSPSQNLAYKDKQSYGFPLPTLSSPAAKYDAFLVNMPYPA 760
 QY 721 FKRMDYFHSVLLKTHATBRGNYNVUSGPIEDYDNYDGHFDADEITKHLANTDVPPTHY 780
 Db 761 FKRVNYNFYORVLYKXASRGNVNSCPIFDYDGHDTEDKIQYVEGSSIPVPTHY 820
 QY 781 FVVLQCRNKSHTPENCPWMLDVLPI-PHRPNVNECPEGPEALWYTERTAHTARV 840
 Db 821 YSILTSCLDTQPAKCDQPLSYSSFLPHRPONECNSSEDSESKYEEMLKNTHTARV 880
 QY 841 DVELLTLGDFQDKVQPVBSLQLQTYLPFTETI 875
 Db 881 DIEHTLSDFERKTSRSYFEILTKLYHTYESEI 915

RESULT 12
 US-08-346-455B-34
 ; Sequence 34, Application US/08346455B
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOILITY STIMULATING
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; NUMBER OF INVENTION: THERAPY
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEMAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/346-455B
 ; FILING DATE: 28-NOV-1994
 ; CLASSIFICATION: 510
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/06613
 ; FILING DATE: 24-MAY-1995
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249,182
 ; FILING DATE: 25-MAY-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/822,043

FILING DATE: 17-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AUTH
 REGISTRATION NUMBER: 36, 434
 REFERENCE/DOCKET NUMBER: 2026-4149PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-8800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 829
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Unknown
 MOLECULE TYPE: Protein
 HYPOTHETICAL: No
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE: Melanoma
 CELL LINE: A2058
 ORGANELLE:
 FEATURE:
 NAME/KEY:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: Putative protein
 US-10-005-456-B-34
 OTHER INFORMATION: sequence of A2058 Autotaxin
 US-10-005-480a-743
 Query Match 40.9%; Score 1964.5; DB 1; Length 829;
 Best Local Similarity 42.4%; Pred. No. 1,2e-182; Mismatches 239; Indels 91; Gaps 10;
 Matches 363; Conservative 164;
 Db 1 CHDDELQKLTARGWBETQRGEVRNEAHCSEDCDCTNQVVKGEHWD 60
 Qy 142 ENCDTAQQSCQPEGFDPYIPLPSMDGFEREYLTYWDITMPNNKLKGIGISKNRY 201
 Db 61 DDEBEIKAAECAGFTRPPLIIFSDGFRASYMKGSKMPTEKLRGKTSYKRPVY 120
 Qy 202 PRKTKPHTYTVTGLYPSHGIIIDNMYDYNLNKNEFNSLSKSEONNPAMWHGQPMWLTAMY 261
 Db 121 PTKTFPNLYTATGTPESRQIVGNSMDYDFDATHLIGREKFNHRMGGQPLWITAK 180
 Qy 262 QGLKAATYFWPOSEVAINGSPSITMPNGSVPPFEEITSLKWLDPKAEPFRFTMVF 321
 Db 181 QSVKAGTFVW-----SVVIPH-----ERRITLWRWLTPDHERESVAFYS 222
 Qy 322 BPDSSCHAGGVSA ----- 336
 Db 223 EQPDEFSKHYSPGPBESYSGPSPFTPAKPKRKRQERPVAPPKKRKRKTHMDHY 282
 Qy 337 -----RVIKALQVVDHAFQMLMEGLKORNHLNCVNNTILLADHGMDDTCYCNRMETMYD 389
 Db 283 AAETRDKMTNPLRERDKTIVQQLDQLKQLRQVNVYFVGHGMEDVTCRTEFLSY 342
 Db 390 FPRINPFFYMBPAPRIR --AHNIPHDPFFSNSEEIVRNLSCKRDPDKDHFKEYLTPDLPK 446
 Db 343 LTNVDDITLPGTGLRIRSKESNNAKYD---PKAIANLNTKPKDHFPRYLQKHLPK 397
 Qy 447 RLHYAKNVRIDKVALFVDOOW-----LAVRSKNTNC_GGGNHGTYNNEFRSMEAFLAH 499
 Db 398 RLHYANRRIEDHILIVERKWHVARKPLDLYKXPSGKCFQGDHGFDKVNSMQTVFGY 457
 Qy 500 GPSFKERKTEVPEPFENIEVNLCDLRLIOPAPNGTHGSLNHLKVPFEYPSHAEEVSKP 559
 Db 458 GPTFKTKTVPFPFENIELTAVMCDLGLKEAPNGTHGSLNHLRNTFRPIMPEEVTR 517

Qy 560 SVCGFANPLPTESDLDCFC - PHLONSTOLEQVNQMLNLTQEELITATVKNLDFGRPRVLQK 618
 Db 518 NYPGIMYLQSDDDDGCTDDKVKPKNQKDELMKRLHTK---GSIEERHLLYGRPAVLYR 573
 Qy 619 NVDHCLLHYREYVSGFGKAMRPMWSSYTPOLGDTPPLPPTVDPDCIRADVTPPSESQK 678
 Db 574 -TRVDILHITDPESGYSEFMLMWTSTVSKQAEVSUPHLSCTVRDPVSPFSQN 632
 Qy 679 CSFYLAQDKNITHGGLYPPASNRTSDSYOALTSNIVPMYREFRKNWDFPSVLLJKHAT 738.
 Db 633 CLAYKNDKNSYGL_FPPUSSPEAKDADFLVNMVPMYPAFKRWNWYQFRLVRYAS 692
 Qy 739 ERGNGVNVSGPPIFYDNGHFDADPDTKHLANTDPIPTHYFWVLTSCKNKSHTPENCP 798
 Db 693 ERGNGVVISCPIDFYDGLHDTEDKQYQVYEGSSTIVPHTYSSITISCLDFTPADKCD 752
 Qy 799 GWLWLPFLPHRPTNVNSCPEGKPEALWVEERFTAHYARVDVLLGDFYQDXVQPV 858
 Db 753 GPLSVSFLPHRDNESSCNNSSEDESKWVSELMQHETARVDIEHLLSDFRKTSRSY 812
 Qy 859 SEILOQKTYLPLPFTTI 875
 Db 813 PEILTKTLYHTVESEI 829

RESULT 13
 US-08-977-221-34
 / Sequence 34, Application US/08977221
 ;
 ; Patent No. 608469
 ; GENERAL INFORMATION:
 ; APPLICANT: UNITED STATES OF AMERICA; DEPT.
 ; APPLICANT: OF HEALTH AND HUMAN SERVICES
 ; TITLE OF INVENTION: MOTILITY STIMULATING
 ; NUMBER OF SEQUENCES: 69
 ; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 ; NUMBER OF SEQUENCES: 69
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US-08/977, 221
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/346, 455
 ; FILING DATE: 28-NOV-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/249, 182
 ; FILING DATE: 25-MAY-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/922, 043
 ; FILING DATE: 17-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DOROTHY R. AUTH
 ; REGISTRATION NUMBER: 36, 434
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4500
 ; TELEFAX: (212) 751-6849
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 829
 ; TYPE: amino acid

RESULT 15
PCT-US95-06613-34
; Sequence 34, Application PC/TUS9506613
; GENERAL INFORMATION:
; APPLICANT: STRACKE, MARY; LIOTTA, LANCE;
; APPLICANT: SCHIFFMANN, ELLIOTT; KRUTSCH,
; APPLICANT: HENRY; MURATA, JUN
; TITLE OF INVENTION: MOTILITY STIMULATING
; TITLE OF INVENTION: PROTEIN USEFUL IN CANCER DIAGNOSIS AND
; NUMBER OF SEQUENCES: 69
; ADDRESSSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/TUS95/06613
; FILING DATE: 24-NOV-1995
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/346,455
; FILING DATE: 28-NOV-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/249,182
; FILING DATE: 25-MAY-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/822,043
; FILING DATE: 17-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36,434
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 929
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Protein
; HYPOTHETICAL: No
; ORIGINATOR SOURCE:
; ORGANISM: Human
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Melanoma
; CELL LINE: A2058
; ORGANELLE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: Putative Protein
; OTHER INFORMATION: sequence of A2058 Autotaxin
; PCT-US95-06613-34

Query Match 40.8%; Score 1964.5%; DB 5; Length 829;
Best Local Similarity 42.4%; Pred. No. 1.2e-182;
Matches 363; Conservative 164; Mismatches 239; Indels 91; Gaps 10;

Qy 82 CWDDEFDCVESTRIWNCNKERCPGETRLEASLCSDDCLQKDCADYKSVCGETSWLE 141
Db 1 CHDFDECLIKTARGNECTKDRGEGVNEAACEDCLRGDCCTNWQVICKGEHWD 60

Qy 142 ENCDTADQSOCPGEFDPPVLFPSMDGFRAEYLWDDTIMPNINKGTHSKYRAMY 201
Db 61 DDECEBKAACEPAGFVRPLIISYDGFRASTYNGKGSKMPNTEKLRSGTISPYMPVY 120

Qy 202 PTKTFPHYHTVLTGYPESHGIGIINNMKVDNLNKNSLSSKEONPAWHGCPMLTAMY 261
Db 121 PTKTFPHYHTVLTGYPESHGIGIINNMKVDNLNKNSLSSKEONPAWHGCPMLTAMY 261

Qy 262 QGKIAATYFWPGSEVAIINGSFPSLYMPYNGSVPPFEERSTLKLWDLPAERPRFTMYF 321
Db 181 QGVRAGTFW-----SVVPH-----ERRLTLRWLTLDPHERPSVTAFYS 222

Qy 322 EBPDSCHAGGPVSA-----336
Db 223 ECPDFSSHKTYKTFGPDESSYGSPTPAKPRQREREPVAPPKRQRERKHHMDHY 282

Qy 337 -----RVIKALQVYDHAFCGMILMEGLIKORNLNHCNVTILLADHGMQDTQCNKMEYMTDY 389
Db 283 AAETRQKMTNPLREIDKTYGQMDGLKOLKLCRVCNTIVFBGDMIDVTCRTEFLSY 342

Qy 390 FPRINFFYMEPGPAPRIR--AHPNIPHDEFFSENSEEVYRNLSCRKPDQHFKPYLTDPLK 446
Db 343 LTNVDDDTLVEGLGRRSKFSNNAKYD----PKAIAANLTKKCPQHFKPYLKQHLPK 397

Qy 447 RHYAKCVRIDKVKHEDQW----LAVRSISNTNC-GGNGHGNNEPFSMEALFLAH 499
Db 398 RHYANRNRDIHULVERWHARKPLDVGKPSGKFFQGDHGFKVNSMOTVFGVY 457

Qy 500 GPSPEKTEVEPFPENIEVNLMDLRLQAPANGTHGSNLHLKPPYFPEPSHAEBVKP 559

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Db 458 GPTFKYKVKVPPFENIELVNWCDLGLKPAAPNGTHGSLNHLRLRNTPTNEEVTRP 517
Qy 560 SVCGFANPLPTESLDCFG-PhiQNSTOLEQYQMINLTLQEBITAVKVNLFGRSPYRQK 618
Db 518 NYFGIMYIQLQDDLGCTDDKVEPKNKLDELNKLHTK---GSTEEFLILYGRPAVLR 573
Qy 619 NVDHCLLYTHREYVSGFGRAMRMPMWSSTYFQLDTSPLPPTVPCCLRADVRVPPSESK 678
Db 574 -TRYDILHATDPSGYSEIFMLLWTSYTVSKQAEVSSVDPHLISCVRPDVVRSPSFQN 632
Qy 679 CSFYLADKNTITHFLYPASNRTSDSOYDALITSLVPMYEEFRKMWDFHESVILLKHAT 738
Db 633 CLAYKNDTOMSIGRLFPYISSLSSPEAKYDALLVINNVPMPAFKRWNTFQRVLUKRYAS 692
Qy 739 ERNGVNVNSGPIFDDYDGHFEDAPDEITKHANTDPIIPTHFWVLTSCRNKSHTPENCP 798
Db 693 ERNGVNVNSGPIFDDYDGLHDTEDK1KQYVEGSSIIPVPHYIISITSCUDFTOPADKD 752
Qy 799 GNDVLPPTIPIRPTANVSCPGKPEALWYERFTAHARVDRVLLTGLDFYDDKVQFV 838
Db 753 GPUSVSSFLPHRPDNECSNSSEDESKWVSELMKQHTARVDRDIEHTSLDFPRXTSRY 812
Qy 859 SEILOQKYLPTBETTI 875
Db 813 PEIITLKYLYTSEI 829

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Search completed: July 6, 2004, 13:21:04
 Job time : 27 secs

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OM protein - protein search, using sw model

Run on: July 6, 2004, 13:19:53 ; Search time 56 Seconds
(without alignments)

Scoring table: BLOSUM62

Title: US-10-005-480A-743

Perfect score: 4804

Sequence: 1 MESTIILATEQPVKNTLKK.QPVSEIIQLQKTYLPTFETTI 875

Scoring table: Gapep 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 45 summaries

Database : Published Applications At: *

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2: /cgn2_6/ptodata/2/pubbaa/2_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/2/pubbaa/1US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubbaa/1US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubbaa/1US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubbaa/1US07_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubbaa/1US09C_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubbaa/1US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubbaa/1US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubbaa/1US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubbaa/1US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubbaa/1US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubbaa/1US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubbaa/1US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4804	100.0	875	14 US-10-062-109A-743	Sequence 743, App
2	4804	100.0	875	14 US-10-062-109A-747	Sequence 747, App
3	4804	100.0	875	14 US-10-062-109A-751	Sequence 751, App
4	4804	100.0	875	14 US-10-005-480A-743	Sequence 743, App
5	4804	100.0	875	14 US-10-005-480A-747	Sequence 747, App
6	4804	100.0	875	14 US-10-005-480A-751	Sequence 751, App
7	4804	100.0	875	15 US-10-291-241-3	Sequence 3, App
8	4804	100.0	875	15 US-10-291-241-11	Sequence 11, App
9	4804	100.0	875	15 US-10-291-241-16	Sequence 16, App
10	4804	100.0	875	15 US-10-191-241-21	Sequence 21, App
11	4804	100.0	875	15 US-10-291-241-22	Sequence 22, App
12	4804	100.0	875	15 US-10-291-241-81	Sequence 81, App
13	4804	100.0	875	15 US-10-291-241-94	Sequence 94, App
14	4804	100.0	875	15 US-10-291-241-95	Sequence 95, App
15	4804	100.0	875	15 US-10-291-241-96	Sequence 96, App

ALIGNMENTS

RESULT 1
US-10-062-109A-743
Sequence 743, Application US/10062109A
Publication No. US20030165505A1
GENERAL INFORMATION:
APPLICANT: Agensys
APPLICANT: Challita-Eld, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REFERENCE: 51158-20062-01
CURRENT APPLICATION NUMBER: US/10/062-109A
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
SEQ ID NO: 743
LENGTH: 875
TYPE: PRT
ORGANISM: Homo sapiens
US-10-062-109A-743
Query Match 100.0%; Score 4804; DB 14; Length 875;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 875; Conservative 0;
SOFTWARE: FastSEQ for Windows Version 4.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1	4804	100.0	875	14 US-10-062-109A-743	Sequence 743, App
2	4804	100.0	875	14 US-10-062-109A-747	Sequence 747, App
3	4804	100.0	875	14 US-10-062-109A-751	Sequence 751, App
4	4804	100.0	875	14 US-10-005-480A-743	Sequence 743, App
5	4804	100.0	875	14 US-10-005-480A-747	Sequence 747, App
6	4804	100.0	875	14 US-10-005-480A-751	Sequence 751, App
7	4804	100.0	875	15 US-10-291-241-3	Sequence 3, App
8	4804	100.0	875	15 US-10-291-241-11	Sequence 11, App
9	4804	100.0	875	15 US-10-291-241-16	Sequence 16, App
10	4804	100.0	875	15 US-10-191-241-21	Sequence 21, App
11	4804	100.0	875	15 US-10-291-241-22	Sequence 22, App
12	4804	100.0	875	15 US-10-291-241-81	Sequence 81, App
13	4804	100.0	875	15 US-10-291-241-94	Sequence 94, App
14	4804	100.0	875	15 US-10-291-241-95	Sequence 95, App
15	4804	100.0	875	15 US-10-291-241-96	Sequence 96, App

61 ASFRGLENCRDVACKDRGCDWFDTCVESTR.IWMNKFRCGTRLLASLCSDDDL 120 ; PRIOR APPLICATION NUMBER: US 10/005, 480
 121 QKRDCCADYKSYCOGETSWLEENCDTAQOSOCPEGFDLPPVILFSMDGFRAEYLTYWDL 180 ; PRIOR FILING DATE: 2001-11-07
 121 QKRDCCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDL 180 ; NUMBER OF SEQ ID NOS: 765
 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240 ; SOFTWARE: FastSEQ for Windows Version 4.0
 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240 ; SEQ ID NO: 747
 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240 ; LENGTH: 875
 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240 ; TYPE: PRT
 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240 ; ORGANISM: Homo sapiens
 US-10-062-109A-747

Query Match 100 0%; Score 4804; DB 14; Length 875;
 Best Local Similarity 100 0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEOPVKCNTLKEYKIACTVLLVIMSLGLGLGLGIRKLEKQGSCRKKCPD 60
 Db 1 MESTLTLATEOPVKCNTLKEYKIACTVLLVIMSLGLGLGLGIRKLEKQGSCRKKCPD 60
 Qy 61 ASFRGLENCRDVACKDRGCDWFDTCVESTR.IWMNKFRCGTRLLASLCSDDDL 120
 Db 61 ASFRGLENCRDVACKDRGCDWFDTCVESTR.IWMNKFRCGTRLLASLCSDDDL 120
 Qy 121 QRKDCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDL 180
 Db 121 QRKDCADYKSYCQGETSWLEENCDTAQOSQCPEGFDLPPVILFSMDGFRAEYLTYWDL 180
 Qy 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240
 Db 181 MPNINKLKTGCIHSKYMRAKYPTKTFPNHYTIVTGLYPSHGI.DNNMVDUNLNKNEFLS 240
 Qy 241 SKEQNPAWHQGPMWLTAMYQGLKAATFWPGSEVATNGFSPTIYMPNGSYPFEBRS 300
 Db 241 SKEQNPAWHQGPMWLTAMYQGLKAATFWPGSEVATNGFSPTIYMPNGSYPFEBRS 300
 Qy 301 TLLKWDLPAERPRFTYMFEEPDSSGAGGPGVSARTIKALQVVDHAFGMLMEGLKORN 360
 Db 301 TLLKWDLPAERPRFTYMFEEPDSSGAGGPGVSARTIKALQVVDHAFGMLMEGLKORN 360
 Qy 361 LANCYNIIILADHGMDQTYCNKMYMTDQFPRINFTYMEGAPRIRAHNIPHDFFNS 420
 Db 361 LANCYNIIILADHGMDQTYCNKMYMTDQFPRINFTYMEGAPRIRAHNIPHDFFNS 420
 Qy 421 BEIVNLSCKRKPDPDKPFLTPDLPKRLHYAKNVRIDKTHLYFDQOQLAVRSKSNTNCGS 480
 Db 421 BEIVNLSCKRKPDPDKPFLTPDLPKRLHYAKNVRIDKTHLYFDQOQLAVRSKSNTNCGS 480
 Qy 481 GNGHYNNEFERSMEAIAFLAHPSPKEKTEVPEPFENIEVNLCDLLRQAPANGTHGSLN 540
 Db 481 GNGHYNNEFERSMEAIAFLAHPSPKEKTEVPEPFENIEVNLCDLLRQAPANGTHGSLN 540
 Qy 541 HLLKYPFDSHAEVSKSVCGANPLPTESLDCFCPHLQNQSTOLEQVNQMLNLTQEET 600
 Db 541 HLLKYPFDSHAEVSKSVCGANPLPTESLDCFCPHLQNQSTOLEQVNQMLNLTQEET 600
 Qy 601 TATYKVNLFGRGRPLQVNQDHCILYHREYVSGKAMRPMWSSTVQPLQDTSPLPPT 660
 Db 601 TATYKVNLFGRGRPLQVNQDHCILYHREYVSGKAMRPMWSSTVQPLQDTSPLPPT 660
 Qy 661 VPDLRADTRVPSESEQCSFYLADKNTTHGFYPPASNRTSDSQDALITSNLYVMYEE 720
 Db 661 VPDLRADTRVPSESEQCSFYLADKNTTHGFYPPASNRTSDSQDALITSNLYVMYEE 720
 Qy 721 FRYKWDYTHSVLJLKHATTERGUNVSGPFDYNYDCHEDADDEITKHLANTDVPJPTV 780
 Db 721 FRYKWDYTHSVLJLKHATTERGUNVSGPFDYNYDCHEDADDEITKHLANTDVPJPTV 780
 Qy 781 FVVLTSCKNSKHTPENCQWLDLPLFSTPHTPTNVSCEPKPEALWVEERFTAHARV 840
 Db 781 FVVLTSCKNSKHTPENCQWLDLPLFSTPHTPTNVSCEPKPEALWVEERFTAHARV 840
 Qy 841 DVLLTGJDFYQDVQPVSEB10LQK1YLPFTETTI 875
 Db 841 DVLLTGJDFYQDVQPVSEB10LQK1YLPFTETTI 875

RESULT 2
 US-10-062-109A-747
 Sequence 747, Application US/10062109A
 Publication No. US201030165505A1
 GENERAL INFORMATION:
 APPLICANT: Agensys
 APPLICANT: Challita-Eld, Pia M.
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Paris, Mary
 APPLICANT: Huber, Rene S.
 APPLICANT: Morrison, Karen Jane Meyrick
 APPLICANT: Jakobovits, Aya
 TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 51158-20062-01
 CURRENT APPLICATION NUMBER: US/10/062,109A
 CURRENT FILING DATE: 2002-01-31

Qy 781 FVVLTSCKNSKHTPENCQWLDLPLFSTPHTPTNVSCEPKPEALWVEERFTAHARV 840
 Db 781 FVVLTSCKNSKHTPENCQWLDLPLFSTPHTPTNVSCEPKPEALWVEERFTAHARV 840
 Qy 841 DVLLTGJDFYQDVQPVSEB10LQK1YLPFTETTI 875
 Db 841 DVLLTGJDFYQDVQPVSEB10LQK1YLPFTETTI 875

RESULT 3							
US-10-062-109A-751 Application US/10062109A Sequence 751 Application US/10062109A ; Publication No. US2003016505A1 ; GENERAL INFORMATION:							
; APPLICANT: Agensys ; APPLICANT: Challita-Eid, Pia M. ; APPLICANT: Raitano, Arthur B. ; APPLICANT: Paris, Mary ; APPLICANT: Hubert, Rene S. ; APPLICANT: Morrison, Karen Jane Meyrick ; APPLICANT: Jakobovits, AyA ; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein ; TITLE OF INVENTION: Entitled 161-P2F10B Useful in Treatment and Detection of ; TITLE OF INVENTION: Cancer ; FILE REFERENCE: 51158-002.01 ; CURRENT APPLICATION NUMBER: US/10/062,109A ; CURRENT FILING DATE: 2002-01-31 ; PRIOR APPLICATION NUMBER: US 10/005,480 ; PRIOR FILING DATE: 2001-11-07 ; NUMBER OF SEQ ID NOS: 765 ; SOFTWARE: Fast-SEQ for Windows Version 4.0 SEQ ID NO 751 LENGTH: 875 ; TYPE: PR ⁺ ; ORGANISM: Homo sapiens							
Qy	1	MESTIITLATEQPKTKNTLKKYKIACTIVLALLIVMSIGLGLGIGKRLBKQGSCRKCFD	60	Score 4804; DB 14; Length 875;	;	;	;
Db	1	MESTIITLATEQPKTKNTLKKYKIACTIVLALLIVMSIGLGLGIGKRLBKQGSCRKCFD	60	;	;	;	;
Qy	61	ASFGLLENRCVDAVKDRGDCWDFFDTCVESTRWMCNKFRGTRLEASLGSDDCI	120	;	;	;	;
Db	61	ASFGLLENRCVDAVKDRGDCWDFFDTCVESTRWMCNKFRGTRLEASLGSDDCI	120	;	;	;	;
Qy	121	QKKDCCADYKSVQCGETSWLBEENCATAQOSQCGPEGFDRPPTVLFMDGFRAYLTYWDTL	180	;	;	;	;
Db	121	QKKDCADYKSVQCGETSWLBEENCATAQOSQCGPEGFDRPPTVLFMDGFRAYLTYWDTL	180	;	;	;	;
Qy	181	MPNINKLTKTGTHSKMRYAMPTKTFPNHYTIVTGLYPSHGRGIDDNMYDVNLINKFNSL	240	;	;	;	;
Db	181	MPNINKLTKTGTHSKMRYAMPTKTFPNHYTIVTGLYPSHGRGIDDNMYDVNLINKFNSL	240	;	;	;	;
Qy	241	SKEQNNPAWHGQPMWLTAMYCGLKARYTFPGSEYATINGSFPSYMPYNGSVPFEERIS	300	;	;	;	;
Db	241	SKEQNNPAWHGQPMWLTAMYCGLKARYTFPGSEYATINGSFPSYMPYNGSVPFEERIS	300	;	;	;	;
Qy	301	TLLKWLDPKAERPRFTMWFPEPDSSGHAGPVSARVIALQVDTAAGMLMEGLKRN	360	;	;	;	;
Db	301	TLLKWLDPKAERPRFTMWFPEPDSSGHAGPVSARVIALQVDTAAGMLMEGLKRN	360	;	;	;	;
Qy	361	LHNCVNILLADIGMDQTYCNKMEYMDYFPRINFFMYSQPAPIRANTPHOFSFNS	420	;	;	;	;
Db	361	LHNCVNILLADIGMDQTYCNKMEYMDYFPRINFFMYSQPAPIRANTPHOFSFNS	420	;	;	;	;
Qy	421	EEITRNLSCRKDPOHFKPFLTPPLKPLHYAKNRDKVHLFVDQWLAWSKNTNCG	480	;	;	;	;
Db	421	EEITRNLSCRKDPOHFKPFLTPPLKPLHYAKNRDKVHLFVDQWLAWSKNTNCG	480	;	;	;	;
Qy	481	GNHGYNNFRSMPAIFIAGHGPSKFKETEVEPFNTLEVNLCDLURIOPAQNNGTHGSIN	540	;	;	;	;
Db	481	GNHGYNNFRSMPAIFIAGHGPSKFKETEVEPFNTLEVNLCDLURIOPAQNNGTHGSIN	540	;	;	;	;
Qy	541	HLLKVPFEPSSHAEVSKFSGANPLPTSLDCFCPHLQNSTOLEQVNQMLNTQBEI	600	;	;	;	;
Db	541	HLLKVPFEPSSHAEVSKFSGANPLPTSLDCFCPHLQNSTOLEQVNQMLNTQBEI	600	;	;	;	;

Qy	601	TATVKVNLPGPRVPLQKNDYHDCCLYHRYVSGCKAMRPMWSYTPQLEDTSPLPPT	660
Dp	601	TATVKVNLPGPRVPLQKNDYHDCCLYHRYVSGCKAMRPMWSYTPQLEDTSPLPPT	660
Qy	661	VPDCIRADVRVPPSESQKCSFYLAQDNKNTHGFLYPPASNRTSDSQYDALITSNLVPWEE	720
Dp	661	VPDCIRADVRVPPSESQKCSFYLAQDNKNTHGFLYPPASNRTSDSQYDALITSNLVPWEE	720
Qy	721	FRKMDYFHSVLLIKHATERNGVNVSQPIFDYNDGHFADPDEITHKLANTDPIPHY	780
Dp	721	FRKMDYFHSVLLIKHATERNGVNVSQPIFDYNDGHFADPDEITHKLANTDPIPHY	780
Qy	781	FVVLTCKNSHTPNCPGWDVPLFTHRPTVNESCPEGKPAALWEEERTFHAIARVR	840
Dp	781	FVVLTCKNSHTPNCPGWDVPLFTHRPTVNESCPEGKPAALWEEERTFHAIARVR	840
Qy	841	DVELLTGDFYQDKYQPVSEILQKTYLPTFETI	875
Dp	841	DVELLTGDFYQDKYQPVSEILQKTYLPTFETI	875
Qy	841	DVELLTGDFYQDKYQPVSEILQKTYLPTFETI	875
Qy	US-10-005-480A-743	RESULT 4	
	Sequence 743; Application US/10005480A		
	PUBLICATION NO. US20030191073A1		
	GENERAL INFORMATION:		
	APPLICANT: Agensys		
	APPLICANT: Challita-Bid, Pia M.		
	APPLICANT: Raitano, Arthur B.		
	APPLICANT: Paris, Mary		
	APPLICANT: Hubert, Rene S.		
	APPLICANT: Morrison, Karen Jane Meyrick		
	APPLICANT: Jakabovits, Aya		
	TITLE OF INVENTION: Nucleic Acid and Corresponding Protein		
	TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection o		
	TITLE OF INVENTION: Cancer		
	FILE REFERENCE: 51158-20062,00		
	CURRENT APPLICATION NUMBER: US/10/005,480A		
	CURRENT FILING DATE: 2001-11-07		
	NUMBER OF SEQ ID NOS: 765		
	SOFTWARE: FastSEQ for Windows Version 4.0		
	SEQ ID NO 743		
	LENGTH: 875		
	TYPE: PRT		
	ORGANISM: Homo Sapien		
	US-10-005-480A-743		
Qy	1	Query Match 100.0%; Score 4804; DB 14; Length 875;	
	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0		
	Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
Qy	1	MESTLTLATEQPVKNTLKKYKIACTIVLLVIMSGLGLKLEKGSKRKCFD 60	
Dp	1	MESTLTLATEQPVKNTLKKYKIACTIVLLVIMSGLGLKLEKGSKRKCFD 60	
Qy	61	ASFRGLENCRDVAACKDRGICCWEDTCYESTIWMCNKFRCETRLEASLCSCDCCL 120	
Dp	61	ASFRGLENCRDVAACKDRGICCWEDTCYESTIWMCNKFRCETRLEASLCSCDCCL 120	
Qy	121	QKKDCCADYKSVCGQETSMLENDTAAQSQCPBGFDLPPVILFMSMDGFRAEVLYTWTDL 180	
Dp	121	QKKDCCADYKSVCGQETSMLENDTAAQSQCPBGFDLPPVILFMSMDGFRAEVLYTWTDL 180	
Qy	181	MPNINKLKTGCIHSKMRAMYPTKTFPHYITIVTGLYPESHGILDNNMYDVNLKNFSL 240	
Dp	181	MENINKLKTGCIHSKMRAMYPTKTFPHYITIVTGLYPESHGILDNNMYDVNLKNFSL 240	
Qy	241	SKEQNPAWHRQPKWLTAMYQGLKATYFWPGSEVAINGSFPIYMPNGSYFEEIRIS 300	
Dp	241	SKEQNPAWHRQPKWLTAMYQGLKATYFWPGSEVAINGSFPIYMPNGSYFEEIRIS 300	
Qy	301	TWKWLDPKAERPREFTYMFEDPDSSHAGGPYSARVIALQVTDHAFGMLMEGLKORN 360	

Db 301 TLLKWLDPKAEPRPYTMVFEPPSSGHAGGPYSARYTKALQYVDHAFGMLMEGLKQRN 360
 Qy 361 LHNCVNLLILLADHGMDQTYCNRMEMTIDYPRINFFYMEPPGAPRIRAHNI PHDFFSENS 420
 Db 361 LHNCVNLLILLADHGMDQTYCNRMEMTIDYPRINFFYMEPPGAPRIRAHNI PHDFFSENS 420
 Qy 421 EBI1VRNLSCKRPDQHKPVLTPDLPKRLHYAKNVRIDKVLFLFDQDQNLAVRSKSNTNCGG 480
 Db 421 EBI1VRNLSCKRPDQHKPVLTPDLPKRLHYAKNVRIDKVLFLFDQDQNLAVRSKSNTNCGG 480
 Qy 481 GNHGYNNEFRSMEAFLAHPGSFKEKTEVPPFENIEVNLCDLLR10PAPNGTHCSL 540
 Db 481 GNHGYNNEFRSMEAFLAHPGSFKEKTEVPPFENIEVNLCDLLR10PAPNGTHCSL 540
 Qy 541 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Db 541 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Qy 601 TATVKYNLPFSPRVRVQYDHC1LYHREYSGFKAMKMPMSSYTVPLQGDTSPLPPT 660
 Db 601 TATVKYNLPFSPRVRVQYDHC1LYHREYSGFKAMKMPMSSYTVPLQGDTSPLPPT 660
 Qy 661 VPDCLERADVRVPPBSSQCSFYLADK1NTHGFLYPPASNRTSQDQYDAL1TSLNVPNEYE 720
 Db 661 VPDCLERADVRVPPBSSQCSFYLADK1NTHGFLYPPASNRTSQDQYDAL1TSLNVPNEYE 720
 Qy 721 FRKMDYFHSVLLIKHATEBANGUNVSGP1F6DNYDGFHDAPD1TKLANTDVP1FTHY 780
 Db 721 FRKMDYFHSVLLIKHATEBANGUNVSGP1F6DNYDGFHDAPD1TKLANTDVP1FTHY 780
 Qy 781 FVVLTSCKNSHTPENCPGHLQDVPF1IIPRPTVNECPEGKPEALWTERTAH1ARVR 840
 Db 781 FVVLTSCKNSHTPENCPGHLQDVPF1IIPRPTVNECPEGKPEALWTERTAH1ARVR 840
 Qy 841 DVELLTGLDFQDKVQPVSE1LQLKTYLPTFETTI 875
 Db 841 DVELLTGLDFQDKVQPVSE1LQLKTYLPTFETTI 875

RESULT 5

US-10-005-480A-747
 Sequence 747, Application US/10005480A

Publication No. US20030191073A1

GENERAL INFORMATION:

APPLICANT: Agensys

APPLICANT: Raianao, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Corresponding Protein Software: FastSEQ for Windows Version 4.0

TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

CURRENT APPLICATION NUMBER: US/10/005,480A

NUMBER OF SEQ ID NOS: 765

SEQ ID NO: 747

LENGTH: 875

TYPE: PRT

ORGANISM: Homo Sapien

FILE REFERENCE: 5158-20063.00

CURRENT FILING DATE: 2001-11-07

RESULT 6

US-10-005-480A-751

Sequence 751, Application US/10005480A

Publication No. US20030191073A1

GENERAL INFORMATION:

APPLICANT: Agensys

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Reitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

TITLE OF INVENTION: Cancer

Db 1 MEST1LTLATQPVKNTLKKYKIACTIVALLIYMSLGLGIGLGLKLEQOSCRKCFD 60

Db 1 MEST1LTLATQPVKNTLKKYKIACTIVALLIYMSLGLGIGLGLKLEQOSCRKCFD 60

Qy 61 ASFRGLENCRCDVACKRQGDCWDFFDTCTVESTRIVCNKFRGEGTLEASLCSCSDCL 120
 Db 61 ASFRGLENCRCDVACKRQGDCWDFFDTCTVESTRIVCNKFRGEGTLEASLCSCSDCL 120
 Qy 121 QKDKCCADYKSVCOGETSWLEENCDTACQOSCPEGFLPPVTFMSDGFRAEYLTVWDTL 180
 Db 121 QKDKCCADYKSVCOGETSWLEENCDTACQOSCPEGFLPPVTFMSDGFRAEYLTVWDTL 180
 Qy 181 MPNINKLKTGIGHSKYSKYMAMYPTKTFPNTYH1TVTGLYPESHGIIDINNNYDYNLNQFNSL 240
 Db 181 MPNINKLKTGIGHSKYSKYMAMYPTKTFPNTYH1TVTGLYPESHGIIDINNNYDYNLNQFNSL 240
 Qy 241 SKEQNNPAWPHQGDMWLTAMYQQLKATYFWGSEAYINGSSEPSITMPPNGSVPPFEEFIRIS 300
 Db 241 SKEQNNPAWPHQGDMWLTAMYQQLKATYFWGSEAYINGSSEPSITMPPNGSVPPFEEFIRIS 300
 Qy 301 TLLKWLDPKAEPRFYMYFEPDSDGHAGGPVSARVIALQVVDHAFCMLMEGLKQRN 360
 Db 301 TLLKWLDPKAEPRFYMYFEPDSDGHAGGPVSARVIALQVVDHAFCMLMEGLKQRN 360
 Qy 361 LHNCVNILLADIGMDQTYCNKHEMTOYDYPFPRINFFYMEPPGAPR1RAHNT1PHDFFSPNS 420
 Db 361 LHNCVNILLADIGMDQTYCNKHEMTOYDYPFPRINFFYMEPPGAPR1RAHNT1PHDFFSPNS 420
 Qy 421 EETVRNLSCKRPDQHFKPVLTPDLPKRLHYAKNVRIDKVLFLFDQDQWLAVRSKSNTNCGG 480
 Db 421 EETVRNLSCKRPDQHFKPVLTPDLPKRLHYAKNVRIDKVLFLFDQDQWLAVRSKSNTNCGG 480
 Qy 481 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Db 481 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Qy 541 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Db 541 HLLKVPFYEPHAAEYSKFSVCGFANPLPTESLDFCPFLQHONSTQLEQYQNMNLQEEI 600
 Qy 601 TATVKYNLPFSPRVRVQYDHC1LYHREYSGFKAMKMPMSSYTVPLQGDTSPLPPT 660
 Db 601 TATVKYNLPFSPRVRVQYDHC1LYHREYSGFKAMKMPMSSYTVPLQGDTSPLPPT 660
 Qy 661 VPDCLERADVRVPPBSSQCSFYLADK1NTHGFLYPPASNRTSQDQYDAL1TSLNVPNEYE 720
 Db 661 VPDCLERADVRVPPBSSQCSFYLADK1NTHGFLYPPASNRTSQDQYDAL1TSLNVPNEYE 720
 Qy 721 FRKMDYFHSVLLIKHATEBANGUNVSGP1F6DNYDGFHDAPD1TKLANTDVP1FTHY 780
 Db 721 FRKMDYFHSVLLIKHATEBANGUNVSGP1F6DNYDGFHDAPD1TKLANTDVP1FTHY 780
 Qy 781 FVVLTSCKNSHTPENCPGHLQDVPF1IIPRPTVNECPEGKPEALWTERTAH1ARVR 840
 Db 781 FVVLTSCKNSHTPENCPGHLQDVPF1IIPRPTVNECPEGKPEALWTERTAH1ARVR 840
 Qy 841 DVELLTGLDFQDKVQPVSE1LQLKTYLPTFETTI 875
 Db 841 DVELLTGLDFQDKVQPVSE1LQLKTYLPTFETTI 875

```

FILE REFERENCE: 51158-20062-00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 755
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 751
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-751

Query Match 100.0% Score 4804; P=ed. No. 0
Best Local Similarity 100.0%; Conservative 0; Mismatched
Matches 875; ; SEQ ID NO: 751

Qy      1  MESTLTLATEQPTVKNTLKKYKACIYLALL
Db      1  MESTLTLATEQPTVKNTLKKYKACIYLALL
Qy      61  ASFGLLENCRDQVACKDQGDCWDFFDTCVEE
Db      61  ASFGLLENCRDQVACKDQGDCWDFFDTCVEE
Qy      121  QKDDCCADYTKSVCCGETSWLLENCDTAQQSQ
Db      121  QKDDCCADYTKSVCCGETSWLLENCDTAQQSQ
Qy      181  MPNINKLKLTCGTHSKYKRAMYPTKTFPHYH
Db      181  MPNINKLKLTCGTHSKYKRAMYPTKTFPHYH
Qy      241  SKEQNNPAWPHQGMWLTAMYQGLKAATYFWN
Db      241  SKEQNNPAWPHQGMWLTAMYQGLKAATYFWN
Qy      301  TLLKWLDDLPKAERFPTYMFEEPDSSHAGG
Db      301  TLLKWLDDLPKAERFPTYMFEEPDSSHAGG
Qy      361  LHNCVNTILLADHGMDQTYCNKNEYMTDYPF
Db      361  LHNCVNTILLADHGMDQTYCNKNEYMTDYPF
Qy      421  EEEIVNLSCRKPDQHFKPVLTDPLKRLHYA
Db      421  EEEIVNLSCRKPDQHFKPVLTDPLKRLHYA
Qy      481  GNHGYNNEFSSMEAFLAIGPSFKEKTYEPF
Db      481  GNHGYNNEFSSMEAFLAIGPSFKEKTYEPF
Qy      541  HLLKPFYFPESSQKESVKSGFANPLPTE
Db      541  HLLKPFYFPESSQKESVKSGFANPLPTE
Qy      601  TATVKVNLPLFGRPRVQLQKNDHCLLYREYV
Db      601  TATVKVNLPLFGRPRVQLQKNDHCLLYREYV
Qy      661  VPDCLRADYRVPPESSQKCSFYLADKNITHG
Db      661  VPDCLRADYRVPPESSQKCSFYLADKNITHG
Qy      721  PRKMDYFHSVLLIKAHATERNGVNVSGPFL
Db      721  PRKMDYFHSVLLIKAHATERNGVNVSGPFL
Qy      781  FVVLTSCKNSKHTPENCPGMDVLPFPIPH
Db      781  FVVLTSCKNSKHTPENCPGMDVLPFPIPH
Qy      841  DVEBLTGLDFYDOKTYPVSEILOKTYLPTF

```

RESULT 7
 US-10-291-241-3
 ; Sequence 3, Application US/10291241
 ; Publication No. US201030206905A1
 ; GENERAL INFORMATION:
 ; AGENT: Agensys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Robert Challita-Bid
 ; APPLICANT: M. Challita-Bid
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 51158-20062-20
 ; CURRENT APPLICATION NUMBER: US/10/291,241
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/062,109
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/282,739
 ; PRIOR FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 875
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-291-241-3

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Missmatches 0; Indels 0; Gaps 0;

Qy	1	MESTIITLATEQPYVKNTLKKYKTACTIVALLYIMSTLGIGLGLRKLEKGQGCRKKCFD	60
Db	1	MESTIITLATEQPYVKNTLKKYKTACTIVALLYIMSTLGIGLGLRKLEKGQGCRKKCFD	60
Qy	61	ASPRGLENCRDYACKDRSDCCWDFEDTCVESTRIWMCNKFRGCTTRLEASLCSDDCL	120
Db	61	ASPRGLENCRDYACKDRSDCCWDFEDTCVESTRIWMCNKFRGCTTRLEASLCSDDCL	120
Qy	121	QKDCDADYCKTSVCGETSMLLEENCDTAQSOCPCBGFDLPPVILSMGDFRAEYLWTDL	180
Db	121	QKDCDADYCKTSVCGETSMLLEENCDTAQSOCPCBGFDLPPVILSMGDFRAEYLWTDL	180
Qy	181	MPNINKLKTGIGHSKSYMRANYPTKTFPNHYTIVGLYPESHGIIIDNNYDVNLNKNFSL	240
Db	181	MPNINKLKTGIGHSKSYMRANYPTKTFPNHYTIVGLYPESHGIIIDNNYDVNLNKNFSL	240
Qy	241	SKEQNPNPAWNGQPMWLTAMYQGKKAATYFWPGSEVAINGSFPSSYMPNGSYPEERIS	300
Db	241	SKEQNPNPAWNGQPMWLTAMYQGKKAATYFWPGSEVAINGSFPSSYMPNGSYPEERIS	300
Qy	301	TLLKIDLPLKAERPFYTMFEPPSSGAGGPYSARVIKALQVTDHAFGMLMEGKQRM	360
Db	301	TLLKIDLPLKAERPFYTMFEPPSSGAGGPYSARVIKALQVTDHAFGMLMEGKQRM	360
Qy	361	LHNCVNTILLADHGMQDTYCNKQYMTDYPRTINFYMEGAPPTRAINIIPHDFSFNS	420
Db	361	LHNCVNTILLADHGMQDTYCNKQYMTDYPRTINFYMEGAPPTRAINIIPHDFSFNS	420
Qy	421	EEIVNLSCKRPDOHFKPLTPDLPLRKYACVTRIDVKYLFDQWMLAVRSKSNTNCGG	480
Db	421	EEIVNLSCKRPDOHFKPLTPDLPLRKYACVTRIDVKYLFDQWMLAVRSKSNTNCGG	480

481 GNGYNNFRSMEAFLANGPSFKERTEVEPFENIEVNLMCDLRLIQAPANNNGTHGSLN 540
 481 GNGYNNFRSMEAFLANGPSFKERTEVEPFENIEVNLMCDLRLIQAPANNNGTHGSLN 540
 541 HLLKYPFYEESSHAEVSKSVCGRANPLTESLDCFCHLQNLSTQLEQYNCMLNLTQEEI 600
 541 HLLKYPFYEESSHAEVSKSVCGRANPLTESLDCFCHLQNLSTQLEQYNCMLNLTQEEI 600
 601 TATVKYLNPFGRPRVLYQKNDHCLLYHREYVSGFGKAMRMKPMNSSYTVPQGDTSPLPPT 660
 601 TATVKYLNPFGRPRVLYQKNDHCLLYHREYVSGFGKAMRMKPMNSSYTVPQGDTSPLPPT 660
 661 VPDCLRADRVPPSEOKCSFYLADKNLTHGFLYPPASNRTESSQYDALITSNLVPMYE 720
 661 VPDCLRADRVPPSEOKCSFYLADKNLTHGFLYPPASNRTESSQYDALITSNLVPMYE 720
 721 FROWDIFYSVLLKHATRNGNVSGI FDNYDGFDADEITGHLLANTDVP IPTHY 780
 721 FROWDIFYSVLLKHATRNGNVSGI FDNYDGFDADEITGHLLANTDVP IPTHY 780
 781 FVVLTSCKRSHPENCPWLDVLPF11PHRPTNVESSPGKPEALWVERFTAHIAVR 840
 781 FVVLTSCKRSHPENCPWLDVLPF11PHRPTNVESSPGKPEALWVERFTAHIAVR 840
 841 DVELLTGLDFYQDKVQPVSEIQLKTYLPTFETTI 875
 841 DVELLTGLDFYQDKVQPVSEIQLKTYLPTFETTI 875
 841 DVELLTGLDFYQDKVQPVSEIQLKTYLPTFETTI 875

RESULT 8

US-10-291-241-11
 Sequence 11, Application US/10291241
 Publication No. US20030206905A1
 GENERAL INFORMATION:
 i APPLICANT: Agensys, Inc.
 i APPLICANT: Aya Jakobovits
 i APPLICANT: Arthur B. Raitano
 i APPLICANT: Mary Faris
 i APPLICANT: Rene S. Hubert
 i APPLICANT: Wangmao Ge
 i APPLICANT: Karen Jane Meyrick Morrison
 i APPLICANT: Robert Kendall Morrison
 i APPLICANT: Pia M. Chaillita-Bid
 i TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 i TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 i TITLE OF INVENTION: CANCER
 i FILE REFERENCE: 5115-B-20062-20
 CURRENT APPLICATION NUMBER: 2003-03-18
 CURRENT FILING DATE: 2003-03-18
 PRIORITY NUMBER: US 10/005,480
 PRIORITY FILING DATE: 2001-11-07
 PRIORITY NUMBER: US 10/062,109
 PRIORITY FILING DATE: 2002-01-31
 PRIORITY NUMBER: US 60/282,739
 NUMBER OF SEQ ID NOS: 103
 SEQ ID NO: 11
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Homo Sapiens

US-10-291-241-11

SEQUENCE 11, Application US/10291241

; Publication No. US20030206905A1

; GENERAL INFORMATION:

; APPLICANT: Agensys, Inc.

; APPLICANT: Aya Jakobovits

; APPLICANT: Arthur B. Raitano

; APPLICANT: Mary Faris

; APPLICANT: Rene S. Hubert

; APPLICANT: Wangmao Ge

; APPLICANT: Karen Jane Meyrick Morrison

; APPLICANT: Robert Kendall Morrison

; APPLICANT: Pia M. Chaillita-Bid

; TITL OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 5115-B-20062-20

CURRENT APPLICATION NUMBER: US/10/291,241
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/005,480
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 10/062,169
 PRIOR FILING DATE: 2002-01-11
 PRIOR APPLICATION NUMBER: US 60/282,739
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 103
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 16
 LENGTH: 875
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-291-241-16

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEQPYKTKTIIKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60
 Db 1 MESTLTLATEQPYKTKTIIKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60

Qy 61 ASPLGLENCRCDYACKDGCDCMDFEDTCVESTRIMNKFCGETRLAESUCS3DDCL 120
 Db 61 ASPLGLENCRCDYACKDGCDCMDFEDTCVESTRIMNKFCGETRLAESUCS3DDCL 120

Qy 121 QKDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180
 Db 121 QKDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180

Qy 181 MPNINKLTKTIGHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240
 Db 181 MPNINKLTKTIGHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240

Qy 241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300
 Db 241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300

Qy 301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360
 Db 301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360

Qy 361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420
 Db 361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420

Qy 421 EETVNLSLCKPDQHCKYITBLPKRYHYAKVBDYQDQMLAVRSKSNTNGG 480
 Db 421 EETVNLSLCKPDQHCKYITBLPKRYHYAKVBDYQDQMLAVRSKSNTNGG 480

Qy 481 GNGHYNNEFRSMEAFLAIGPSFKETKEVPEFENIEVNLMCDLILCQAPANGTHGSLN 540
 Db 481 GNGHYNNEFRSMEAFLAIGPSFKETKEVPEFENIEVNLMCDLILCQAPANGTHGSLN 540

Qy 541 HLLKVPFYEPFSAEFSVCGFANPLPTESLDCFCPHLONSTOLEVNQMLNLTQEBI 600
 Db 541 HLLKVPFYEPFSAEFSVCGFANPLPTESLDCFCPHLONSTOLEVNQMLNLTQEBI 600

Qy 601 TATVKVNLPFGRPYRVLQKNDHCLYHREYSGFGKAHRMPMWSSTYTPQGLDTSPLPPT 660
 Db 601 TATVKVNLPFGRPYRVLQKNDHCLYHREYSGFGKAHRMPMWSSTYTPQGLDTSPLPPT 660

Qy 661 VPDCLRADYRVPSSSQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSULVPMYEE 720
 Db 661 VPDCLRADYRVPSSSQKCSFYLADKNITHGFLYPPASRTSDQYDALITSULVPMYEE 720

Qy 721 FRKMDYFHSSVLLKTAHTERGVNVYSGPFDYNYDGHDADEBTKHLANTDVPYIPTHY 780
 Db 721 FRKMDYFHSSVLLKTAHTERGVNVYSGPFDYNYDGHDADEBTKHLANTDVPYIPTHY 780

Qy 781 FVVLTSCKNSHTPENCPGMUDLPLF1IHPHPTNVECPGKPBALWVEERPAHIAVR 840
 Db 781 FVVLTSCKNSHTPENCPGMUDLPLF1IHPHPTNVECPGKPBALWVEERPAHIAVR 840

RESULT 10
 US-10-291-241-21
 ; Sequence 21, Application US/10291241
 ; Publication No. US2004020605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agenys, Inc.
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Fazis
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wanchao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 51158-200612-20
 ; CURRENT APPLICATION NUMBER: US/10/291,241
 ; PRIORITY APPLICATION NUMBER: US 10/005,480
 ; PRIORITY FILING DATE: 2001-11-07
 ; PRIORITY FILING DATE: 2002-01-31
 ; PRIORITY FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 21
 ; LENGTH: 875
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-291-241-21

Query Match 100.0%; Score 4804; DB 15; Length 875;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60
 Db 1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60

Qy 121 QKDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180
 Db 121 QKDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180

Qy 181 MPNINKLTKTIGHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240
 Db 181 MPNINKLTKTIGHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240

Qy 241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300
 Db 241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300

Qy 301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360
 Db 301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360

Qy 361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420
 Db 361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420

Qy 421 EETVNLSLCKPDQHCKYITBLPKRYHYAKVBDYQDQMLAVRSKSNTNGG 480
 Db 421 EETVNLSLCKPDQHCKYITBLPKRYHYAKVBDYQDQMLAVRSKSNTNGG 480

Qy 481 GNGHYNNEFRSMEAFLAIGPSFKETKEVPEFENIEVNLMCDLILCQAPANGTHGSLN 540
 Db 481 GNGHYNNEFRSMEAFLAIGPSFKETKEVPEFENIEVNLMCDLILCQAPANGTHGSLN 540

Qy 541 HLLKVPFYEPFSAEFSVCGFANPLPTESLDCFCPHLONSTOLEVNQMLNLTQEBI 600
 Db 541 HLLKVPFYEPFSAEFSVCGFANPLPTESLDCFCPHLONSTOLEVNQMLNLTQEBI 600

Qy 601 TATVKVNLPFGRPYRVLQKNDHCLYHREYSGFGKAHRMPMWSSTYTPQGLDTSPLPPT 660
 Db 601 TATVKVNLPFGRPYRVLQKNDHCLYHREYSGFGKAHRMPMWSSTYTPQGLDTSPLPPT 660

Qy 661 VPDCLRADYRVPSSSQKCSFYLADKNITHGFLYPPASNRTSDSQYDALITSULVPMYEE 720
 Db 661 VPDCLRADYRVPSSSQKCSFYLADKNITHGFLYPPASRTSDQYDALITSULVPMYEE 720

Qy 721 FRKMDYFHSSVLLKTAHTERGVNVYSGPFDYNYDGHDADEBTKHLANTDVPYIPTHY 780
 Db 721 FRKMDYFHSSVLLKTAHTERGVNVYSGPFDYNYDGHDADEBTKHLANTDVPYIPTHY 780

Qy 781 FVVLTSCKNSHTPENCPGMUDLPLF1IHPHPTNVECPGKPBALWVEERPAHIAVR 840
 Db 781 FVVLTSCKNSHTPENCPGMUDLPLF1IHPHPTNVECPGKPBALWVEERPAHIAVR 840

1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60
 1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60

1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60
 1 MESTLTLATEQPKTNTLKYKIACTIVALLVIMSIGLGIGLRLKEQGSCRKCFD 60

61 ASFRGLENCRCDVACKDGRGDCMDFEDTCVESTRIMNKFCRGTRLEASLCS3DDCL 120
 61 ASFRGLENCRCDVACKDGRGDCMDFEDTCVESTRIMNKFCRGTRLEASLCS3DDCL 120

121 QKDDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180
 121 QKDDCCADYKSVCOGETSWLEENCDTAQOSCPBEGFLLPPVILFSMDGFRAYLYTWDTL 180

181 MENINLKLTGTHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240
 181 MENINLKLTGTHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240

181 MENINLKLTGTHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240
 181 MENINLKLTGTHSKYMRAAMYPTKTFPHTYITVGLYPSHSGIDINNMYDNLNKNFSL 240

241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300
 241 SKEQNNPAWTHGQPNWLTAMYQIGKAAFYWPSEEVANGSFPSIYMPNGSVPFEERIS 300

301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360
 301 TLLKWLDEPKAERPRFTYMFEEFDSSHAGGGVSARYKALQYDVFHGMIMEGLKQRN 360

361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420
 361 LHNCVNIIILADHENDQTYCNRKHEYMTDIFPRINFYMEGAPRRAHNIPHDFFSFNS 420

Query 421 EETVRNLSCKRPDOHKPKYLTDPDLPKR;HYAKNVRIDKWHLYDQWNLAVRSKSNTNCGG 480
 Database 421 EETVRNLSCKRPDOHKPKYLTDPDLPKR;HYAKNVRIDKWHLYDQWNLAVRSKSNTNCGG 480
 Query 481 GNGHGNNEFRSMEAIFLAGPSFCEKTEVFPENIEVNLMDLRLQAPAPNGTRGSILN 540
 Database 481 GNGHGNNEFRSMEAIFLAGPSFCEKTEVFPENIEVNLMDLRLQAPAPNGTRGSILN 540
 Query 541 HLLKVPFFYBSHAREVSKEVSVCGANPLTESLDCFCFLQNSTQLEBVONMNLQTEI 600
 Database 541 HLLKVPFFYBSHAREVSKEVSVCGANPLTESLDCFCFLQNSTQLEBVONMNLQTEI 600
 Query 601 TATVKVNLDPGRPRVPLQNVNDCLYLHREYVSGFGKAMRMENWSSYTVPLQGDTSPLPPT 660
 Database 601 TATVKVNLDPGRPRVPLQNVNDCLYLHREYVSGFGKAMRMENWSSYTVPLQGDTSPLPPT 660
 Query 661 VPDCLRADRVPPBESQCKSFLYADKNTTHGFLYPPASNRTSDSYDALITSNLVPMYE 720
 Database 661 VPDCLRADRVPPBESQCKSFLYADKNTTHGFLYPPASNRTSDSYDALITSNLVPMYE 720
 Query 721 FRKWDYFHSVLLJLKHATRNGTNNVSGSPIDTYDGHFADADEITHHLANTDVP1PHTY 780
 Database 721 FRKWDYFHSVLLJLKHATRNGTNNVSGSPIDTYDGHFADADEITHHLANTDVP1PHTY 780
 Query 781 FVVLTSCKRKSHTPBNCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Database 781 FVVLTSCKRKSHTPBNCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Query 841 DVELLTGFLYQKQVQPSSEILQKTLPLPFETI 875
 Database 841 DVELLTGFLYQKQVQPSSEILQKTLPLPFETI 875
 Query 841 DVELLTGFLYQDVKVQVPSSEILQKTLPLPFETI 875
 Database 841 DVELLTGFLYQDVKVQVPSSEILQKTLPLPFETI 875

RESULT 11
 US-10-291-241-22
 Sequence 22, Application US/10291241
 Publication No. US20030206905A1
 GENERAL INFORMATION:
 ; APPLICANT: Agensys, Inc.
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Challita-Bid
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 161P2F10B USEFUL IN TREATMENT AND DETECTION OF
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 51158-20062-20
 ; CURRENT APPLICATION NUMBER: US/10/291,241
 ; CURRENT FILING DATE: 2003-03-18
 ; PRIOR APPLICATION NUMBER: US 10/005,480
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/062,109
 ; PRIOR FILING DATE: 2002-01-31
 ; PRIOR APPLICATION NUMBER: US 60/282,739
 ; PRIOR FILING DATE: 2001-04-10
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 875
 ; ORGANISM: Homo Sapiens

Query Match Similarity 100.0%; Score 4804; DB 15; Length 875;
 Best Local Matches 875; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query 1 MESTLILATEQVKNTLKYKIAIVLILIVMSLGLGLGLRDKQGSCRKCFD 60

Db 1 MESTLILATEQVKNTLKYKIAIVLILIVMSLGLGLGLRDKQGSCRKCFD 60
 Qy 61 ASFRGLENCRCDVACKDRGDCWDFBETCYESTRWMCNKFRGCBTRLEASLSCSDCL 120
 Db 61 ASFRGLENCRCDVACKDRGDCWDFBETCYESTRWMCNKFRGCBTRLEASLSCSDCL 120
 Qy 121 QKRDCCADYKSVCQGETSNLEENCDAQSQCPGFDLPPVILFSMDGFRAEVLYTWTDL 180
 Db 121 QKRDCCADYKSVCQGETSNLEENCDAQSQCPGFDLPPVILFSMDGFRAEVLYTWTDL 180
 Qy 181 MPNINKLKTGITHSKYMRAMYPTKFPHNTIVTGLYPSHGLDNNNTDVNLNKNTFLS 240
 Db 181 MPNINKLKTGITHSKYMRAMYPTKFPHNTIVTGLYPSHGLDNNNTDVNLNKNTFLS 240
 Qy 241 SKEQNINPAWHGQPKWMLTAMYQGLKATFWPGSEVAINGSFPSIYKPGNSYFFERIS 300
 Db 241 SKEQNINPAWHGQPKWMLTAMYQGLKATFWPGSEVAINGSFPSIYKPGNSYFFERIS 300
 Qy 301 TLKWLDDPLKAERPRFTYFEEPDSSGHAGGPGVSARYTIALQVDFHAGMMEGLKORN 360
 Db 301 TLKWLDDPLKAERPRFTYFEEPDSSGHAGGPGVSARYTIALQVDFHAGMMEGLKORN 360
 Qy 361 LHNCVNILLADHOMDQTYCNKNEYMTYFPRINNFYMEGPPARIKHNIPDFFSFNS 420
 Db 361 LHNCVNILLADHOMDQTYCNKNEYMTYFPRINNFYMEGPPARIKHNIPDFFSFNS 420
 Qy 421 EETVRNLSCKRKPDKDHFKPLTDPDKLRLHYAKNVRIDKHLFQDQYKLAVRSKSNTNCGG 480
 Db 421 EETVRNLSCKRKPDKDHFKPLTDPDKLRLHYAKNVRIDKHLFQDQYKLAVRSKSNTNCGG 480
 Qy 481 GHGYNNEFRSMEAIFLAGPSFKEKEVPPENIENYLNMDLRLTQAPANGTHGSILN 540
 Db 481 GHGYNNEFRSMEAIFLAGPSFKEKEVPPENIENYLNMDLRLTQAPANGTHGSILN 540
 Qy 541 HLLKVPFYPSPHAEEVSKFSVCCFANPLPTESDCFPHLQNSTQLEQVNQMLNLQTEI 600
 Database 541 HLLKVPFYPSPHAEEVSKFSVCCFANPLPTESDCFPHLQNSTQLEQVNQMLNLQTEI 600
 Qy 601 TATVKVNLPPGRPRVLOKNVDHLCLLYREYVSGFGRKAMRMPKWSSTYVPOLGDTSPLPPT 660
 Database 601 TATVKVNLPPGRPRVLOKNVDHLCLLYREYVSGFGRKAMRMPKWSSTYVPOLGDTSPLPPT 660
 Qy 661 VPDCLRADYRVPPESEQCSFYLADKNTTHGFLYPPASNRTSDSYDALITSNLVPMYE 720
 Database 661 VPDCLRADYRVPPESEQCSFYLADKNTTHGFLYPPASNRTSDSYDALITSNLVPMYE 720
 Qy 721 FVVLTSCKRKSHTPENCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Database 721 FVVLTSCKRKSHTPENCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Qy 781 FVVLTSCKRKSHTPENCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Database 781 FVVLTSCKRKSHTPENCPGWLDPFLP1PHRPNVESCPEGKPEALWVEERTAHARVR 840
 Qy 841 DVELLTGFLDQDKVQVPSSEILQKTLPLPFETI 875
 Database 841 DVELLTGFLDQDKVQVPSSEILQKTLPLPFETI 875
 ; RESULT 12
 ; Sequence 81, Application US/10291241
 ; Publication No. US20030206905A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aya Jakobovits
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison
 ; APPLICANT: Pia M. Challita-Bid
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Arthur B. Raitano
 ; APPLICANT: Mary Paris
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Wangmao Ge
 ; APPLICANT: Karen Jane Meyrick Morrison
 ; APPLICANT: Robert Kendall Morrison

DB	Query Match	Score	DB 15;	Length
301	TUJKWDLPAERPRFTYMFEBPDSGGHAGGPVSARVIKALQVVDHAFCMLMEGLKORN	360	100.0%	875;
361	LHNCVNNTILLADHGMOTYCNKEMYMTDYPRINFFYMEGAPRIRAHNIPHDFFSFNS	420	Best Local Similarity	100.0%;
361	LHNCVNNTILLADHGMOTYCNKEMYMTDYPRINFFYMEGAPRIRAHNIPHDFFSFNS	420	Pred. No. 0;	
361	Matches 875; Conservative 0; Mismatches			
Qy	1 MESTUTLATEQPKVKNTLKKYKIAVICVJALLIVMSIGIGIGLRLKLEKGOSCRKCKPD	60		
Db	1 MESTUTLATEQPKVKNTLKKYKIAVICVJALLIVMSIGIGIGLRLKLEKGOSCRKCKPD	60		
Qy	61 ASFRLGENCQDVACKDRCGCDMDEEDTCVESTRIMCNKFCGETRLEASLSCSDCL 120			
Db	61 ASFRLGENCQDVACKDRCGCDMDEEDTCVESTRIMCNKFCGETRLEASLSCSDCL 120			
Qy	61 ASFRLGENCQDVACKDRCGCDMDEEDTCVESTRIMCNKFCGETRLEASLSCSDCL 120			
Db	121 QKKDCADYKSVQCGETSMILEENCDAQSQCPGFDLPPVILFSMDGRAEYLYTWDTL 180			
Db	121 QKKDCADYKSVQCGETSMILEENCDAQSQCPGFDLPPVILFSMDGRAEYLYTWDTL 180			
Qy	181 MPNTNRLKTCGIGHSKYMRAKYPTKTFPNHYTIVGLYPBSHGIIIDNNNNYDVNLUKNFSLIS	240		
Db	181 MPNTNRLKTCGIGHSKYMRAKYPTKTFPNHYTIVGLYPBSHGIIIDNNNNYDVNLUKNFSLIS	240		
Qy	181 MPNTNRLKTCGIGHSKYMRAKYPTKTFPNHYTIVGLYPBSHGIIIDNNNNYDVNLUKNFSLIS	240		
Db	241 SKEQNPAWQHGPQPMWLTAMYQGKATAFWPGSEVAINGSFPSIYMPYNGSPPFERIS 300			
Db	241 SKEQNPAWQHGPQPMWLTAMYQGKATAFWPGSEVAINGSFPSIYMPYNGSPPFERIS 300			
Qy	301 TLLKWLDLKXERFRFTYMFEEEDDSCHAGGPGSARVTKALQVDHAFCMLMEGLKORN 360			
Db	301 TLLKWLDLKXERFRFTYMFEEEDDSCHAGGPGSARVTKALQVDHAFCMLMEGLKORN 360			
Qy	361 LHNCVNNTILLADHGMOTYCNKEMYMTDYPRINFFYMEGAPRIRAHNIPHDFFSFNS 420			
Db	361 LHNCVNNTILLADHGMOTYCNKEMYMTDYPRINFFYMEGAPRIRAHNIPHDFFSFNS 420			
Qy	421 EETIVNLSCRKPDQHFKPYLTDPLPKRLHYAKNTRIDKTHFLFDQONLAVRSKSNTNGG 480			
Db	421 EETIVNLSCRKPDQHFKPYLTDPLPKRLHYAKNTRIDKTHFLFDQONLAVRSKSNTNGG 480			
Qy	481 GNHGYNNERPSMEALFLAHPSPFKEKTEPEPENIETVNLCDLRLTOPAPNGTHGSLN 540			
Db	481 GNHGYNNERPSMEALFLAHPSPFKEKTEPEPENIETVNLCDLRLTOPAPNGTHGSLN 540			
Qy	541 HLLKVPFEPSPHAEBSKPSVCGFANPLPTESLDCFCPHLQNQSTQLEQYQNMNLQTEEI 600			
Db	541 HLLKVPFEPSPHAEBSKPSVCGFANPLPTESLDCFCPHLQNQSTQLEQYQNMNLQTEEI 600			
Qy	601 TATVKVNLPFGPRVPLVQKQVHCKLHYAKNTRIDKTHFLFDQONLAVRSKSNTNGG 480			
Db	601 TATVKVNLPFGPRVPLVQKQVHCKLHYAKNTRIDKTHFLFDQONLAVRSKSNTNGG 480			
Qy	661 VPDC1RADYRVPSEOKCSFYLADKNITGFLYPASNRTSDSQYDALITSNLVPMYE 720			
Db	661 VPDC1RADYRVPSEOKCSFYLADKNITGFLYPASNRTSDSQYDALITSNLVPMYE 720			
Qy	721 FRIKMDYFHSVLLIKEATERGVNTVSGPFLFDYNDGHDAPDEITKHLANTDPIHTY 780			
Db	721 FRIKMDYFHSVLLIKEATERGVNTVSGPFLFDYNDGHDAPDEITKHLANTDPIHTY 780			
Qy	781 FVVLTSCKNKSHTPENCPGMWDVLPFIIIPRPTNVESCPCKPEALWVERFTAHIAVR 840			
Db	781 FVVLTSCKNKSHTPENCPGMWDVLPFIIIPRPTNVESCPCKPEALWVERFTAHIAVR 840			
Qy	841 DVELLTSGLDFQDKYQVPSB3LQLKHYLPIFETTI 875			
Db	841 DVELLTSGLDFQDKYQVPSB3LQLKHYLPIFETTI 875			
Qy	Sequence 95, Application US/10291241			
Db	GENERAL INFORMATION:			
Qy	Publication No. US2003206905A1			
Db	APPLICANT: Agensys, Inc.			
Qy	APPLICANT: Aya Jakobovits			
Db	APPLICANT: Arthur B. Raitano			
Qy	APPLICANT: Mary Faris			
Db	APPLICANT: Rene S. Robert			
Qy	APPLICANT: Wangmao Ge			
Db	APPLICANT: Karen Jane Meyrick Morrison			
Qy	APPLICANT: Robert Kendall Morrison			
Db	APPLICANT: Robert Kendall Morrison			
Qy	721 PRKMDYFHSVLLIKEATERGVNTVSGPFLFDYNDGHDAPDEITKHLANTDPIHTY 780			
Db	721 PRKMDYFHSVLLIKEATERGVNTVSGPFLFDYNDGHDAPDEITKHLANTDPIHTY 780			
Qy	781 FVVLTSCKNKSHTPENCPGMWDVLPFIIIPRPTNVESCPCKPEALWVERFTAHIAVR 840			
Db	781 FVVLTSCKNKSHTPENCPGMWDVLPFIIIPRPTNVESCPCKPEALWVERFTAHIAVR 840			
Qy	841 DVELLTSGLDFQDKYQVPSB3LQLKHYLPIFETTI 875			
Db	841 DVELLTSGLDFQDKYQVPSB3LQLKHYLPIFETTI 875			

RESULT 15
US-10-291-241-96
; Sequence 96, Application US/10291241
; Publication No. US20130206905A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Aya Jakubovits
; APPLICANT: D. Peter
; APPLICANT: David L. Dabholkar
; APPLICANT: David L. Dabholkar

ENTRANCE NUMBER: 100-00021, 35 JUN 2024, 17:55
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO: 95
LENGTH: 875
TYPE: PR
ORGANISM: Homo Sapiens
S-10-291-241-95

APPLICANT: Mary Paris
 APPLICANT: Rene S. Hubert
 APPLICANT: Wangmao Ge
 APPLICANT: Karen Jane Meyrick Morrison
 APPLICANT: Robert Kendall Morrison
 APPLICANT: Pia M. Challala-Eid
 TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 TITLE OF INVENTION: ENTITLED 161P210B USEFUL IN TREATMENT AND DETECTION OF
 TITLE OF INVENTION: CANCER
 FILE REFERENCE: 51158-20062-20
 CURRENT APPLICATION NUMBER: US/10/291,241
 CURRENT FILING DATE: 2003-03-18
 PRIOR APPLICATION NUMBER: US 10/005,480
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 10/062,109
 PRIOR FILING DATE: 2002-03-31
 PRIOR APPLICATION NUMBER: US 60/282,739
 PRIOR FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 103
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 96
 LENGTH: 975
 TYPE: PRT
 ORGANISM: Homo Sapiens
 SEQ-10-291-241-96

Qy	661	VPDLRADRVPPESESQCSFYLADKNITHGFLYPPASNRTSDSYDALITSNLYPMYEE	720
Db	661	VPDLRADRVPPESESQCSFYLADKNITHGFLYPPASNRTSDSYDALITSNLYPMYEE	720
Qy	721	FRKWDYFHSVLLKHAERGVNVNSGPIDFYNDGHDAPDEITKHLANTDVP1PHTY	780
Db	721	FRKWDYFHSVLLKHAERGVNVNSGPIDFYNDGHDAPDEITKHLANTDVP1PHTY	780
Qy	781	FVVLTSCKNSKSHPENCGWLDDVLPF1PCHRPTNVESCPEGKPEALWVEERTAHARVR	840
Db	781	FVVLTSCKNSKSHPENCGWLDDVLPF1PCHRPTNVESCPEGKPEALWVEERTAHARVR	840
Qy	841	DYELLTGGLDFYQDKVQPYSEIILQLKTYLPTFETI	875
Db	841	DYELLTGGLDFYQDKVQPYSEIILQLKTYLPTFETI	875

Search completed: July 6, 2004, 13:26:07
Job time: 59 secs

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Db	301	ATLQWDLPKAERPSFYTIVVEPDAGKSGPVSAGVTKALQVLDDAEGMLMEGLKQR	360	A; Status: preliminary
Qy	360	NLHNCVNIIILIAHGDMDQTYCNKEMTYDFPRINFEVNYMEGAPRIBAHTNIPHDFPSFN	419	A; Molecule type: mRNA
Db	361	NLHNCVNIIILIAHGDMDQTYCNKEMTYDFPRINFEVNYMEGAPRIBAHTNIPHDFPSFN	419	A; Residue: 1-80 <BEL>
C; Genetics:				
A; Gene: GDNPL; M651; NPBS				
C; Cross-references: GDB:132615; OMIM:173135				
Db	420	SEBIVRNLSCRKPDQHKPLTDPKPLHYAKNVRIDKVLHFDQMLAVRSKSNTNCG	479	A; Cross-references: GDB:692-6923
Qy	420	SEBIVRNLSCRKPDQHKPLTDPKPLHYAKNVRIDKVLHFDQMLAVRSKSNTNCG	479	A; Maf position: 692-6923
C; Superfamily: nucleotide pyrophosphatases; somatomedin B homology				
C; Keywords: coenzyme A; glycoprotein; phosphoprotein; phosphotriester hydrolase; transmembrane				
F; 77-97 Domain: transmembrane #status Predicted				
F; 104-144 Domain: somatomedin B homology <SBH1>				
F; 145-188 Domain: somatomedin B homology <SBH2>				
F; 179-285,341-477,578-585,543,700-731,748 Binding site: carbohydrate (Asn) (covalent) #status predicted				
F; 255/Binding site: AMP (Thr) (covalent) #status predicted				
Query Match	52.0%	Score 2498.5;	DB 1;	Length 925;
Best Local Similarity	53.1%	Pred. No. 6-169		
Matches 465; Conservative 137; Mismatches 250; Indels 23; Gaps 11;				
Qy	10	EOPVTKR---NTLX---KXKIACTIVLALLYIMSLGFLGLGLRKLKEQGSCRKCFDAS	62	
Db	57	EEPLERKAAARTAKDPTVQKPSCKGCRFERT	116	
Qy	63	FRGLENCRCDVACKDRCGCDWFDCTCYESTRIMMNCFKFRGETRLAESTLCSCSDDCLQK	122	
Db	117	F---GNCRCDAACTVELGNCNCLQDQETCIEPEHIIWTCMKFRGEKLRLTSACSDCDRK	173	
Qy	123	KDCCADYKSVCOGETSNBENCQTAQQSQCQFEGFLDPVFLMSMGRARYLYTDTLMP	182	
Db	174	GDCCUNYSSVCQEBKSWBEPCESSINPQCQAGFEPPTFLSLQFRAYLHTWGGLLP	233	
Qy	183	NINLKLTGIGHSKYMRAAMYPTCFPHNHTIVTGLYBPSKGITIDNMYDYNLNKNPSSLSSK	242	
Db	234	VISKLKCCOTYQMRPVYPTCFPHNHTIVTGLYBPSKGITIDNMYDYNLNKNPSSLSSK	293	
Qy	243	EQNNPAWHRGQPWMLTAMYQGLKAATYFWPQSEVAINGSPSISYMPYNGSPFERRISTL	302	
Db	294	EKENPENYKGEPIWTKYCGULKSCFEPWGSDEVLENGIFDIFYKMYNGSPFERRILAV	353	
Qy	303	LKWLDDPKAERPFYTMVFEPPDSSGAGGPKSARVTKALQVVDHAQGMLMEGLKORNLH	362	
Db	354	LQWQLQPLDPERPFYTYLLEEPDSSGHSYGPSSSEVTKAQRVDGMVGMMDGLKELNLH	413	
Qy	363	NCVNTILLADHGMDQTCNKMBSYMTDFPRINFFYMEGAPRIBAHTNIPHDFPSFN	422	
Db	414	RCLNLILISDHGMEQGSSCKKTYILNCKLGDKVNKIVYGEAARLPSDVPDKYSENYEBS	473	
Qy	423	IVRNLSCKRDPDQHKPLTDPKPLHYAKNVRIDKVLHFDQMLAVRSKSNTNCGSC	481	
Db	474	TARNLSCHEPQNQPKPLKHFPKLHFPAKSDRIEPTFLPDQMLAQNPSERKYCGSG	533	
Qy	482	NHGYNNEFRSMEIAFLAHGSPSKETKEVEPENIEVYNNLMDLRLTQPAQNNTHGSLNH	541	
Db	534	FHGSDNIVNSMQLFVGPGPKFHGEADTENIYNNLMDLRLTQPAQNNTHGSLNH	593	
Qy	542	LKXPFYEPSHAEBVSFSVCGFANPLPTESLDCFC-PHLQNSTOLEVNQMLNLTQEEI	600	
Db	594	600 KLIKXHETLPGYERVLQENTYCLLQHNPQYSDDILPLWATYVDR--NDSFSTD 707		
Qy	601	TATKVNLPFGRPRVQKNDVHCLLYREYTSFGKAMNPWSSYTPOLGTSPLRPT	660	
Db	650	660 KLIKXHETLPGYERVLQENTYCLLQHNPQYSDDILPLWATYVDR--NDSFSTD 707		
Qy	661	VPDCLRADYVRPVPSSEOKCSKSFYLAQKNTGFLYPPASNTSDQY-DALITSNLVPMYE	719	
Db	708	708 FSNLYQDFRIPISPVKCSFTYQKNSGTYSEALLTIVPMYQ	767	
A; Residues: 1-945 <BC>				
A; Status: it is uncertain whether Met-1 or Met-53 is the initiator				
R; Funakoshi, I.; Kato, H.; Horie, K.; Yano, T.; Kobayashi, H.; Inoue, T.; Suzuki				
Arch. Biochem. Biophys. 295, 180-187, 1992				
A; Title: Molecular cloning of cDNAs for human fibroblast nucleotide pyrophosphatase.				
A; Reference number: S21706; MUID:22246539; PMID:131502				
A; Accession: A9216				
A; Status: preliminary				
A; Molecule type: mRNA				
A; Residues: 1-945 <BC>				
A; Status: not compared with conceptual translation				
A; Molecule type: mRNA				
A; Residues: 1-325 <UNI>				
A; Accession: S23587				
A; Molecule type: protein				
A; Residues: 116-121,247-271, 'X', 273-275; 279-280, 'X', 282-283; 303-316; 362-364,449-465,482-				
A; Note: it is uncertain whether Met-1 or Met-53 is the initiator				
R; Belli, S.I.; Godin, J.W.				
Eur. J. Biochem. 226, 433-443, 1994				
A; Title: Biochemical characterization of human PC-1, an enzyme possessing alkaline phosphatase activity				
A; Reference number: S51030; MUID:95094801; PMID:801561				
A; Accession: S51030				

Db	828	PTHFFITLTSCKXDKTSQPLHCEH-LDTLAFILPHRTDNESECVHGRKHDDSSWVEELLMLHR	886	Qy	300	STLWKLDLPAERPRFYTMYFEEPDSSGHAGGPVARSVIALQVWDHAFGMLMEGLKQR	359
Qy	837	ARVDRVELLTGFLDYQDKVQPVSEIQLKTYLPTF	871	Db	333	LAVIEWLQLPSHERRHPTFLYLEPDSGHSGPVSESVIALQVDRVGMMLDGEKDL	392
Db	887	ARITDVEHTIGLSFYQKPVSDILKLTKLPTF	921	Qy	360	NLHNCVNITILLADHGMQDTQCNKMEYMTDYPRINFFMYEGPAPIRAHNTIPDFFFSN	419
RESULT 3				Db	393	GLDKCLNLILLISDHGMEOQSCKXVYLINKYLGDVNNTVKVYGPAAARLPTDVETYSFN	452
A27410		A27410		Qy	420	SEEIVNLNSCRKRPDKQHEKPYLTDLKPLRHLHYAXNVRIDKVHLFVDQOM-LAVRSKNTNC	478
nucleotide diphosphatase (EC 3.6.1.9) - mouse		nucleotide diphosphatase (EC 3.6.1.9) - phosphodiesterase I (EC 3.1.1.1)		Db	453	YEALAKKNSCREEPKHPTFLYKPLKPLRHLAKSDRIPPLTFLDQWQLAQNSPERKYC	512
N/Alternate names: nucleotide pyrophosphatase (mouse)		C/Species: Mus musculus (house mouse)		Qy	479	GGGNHGYNNERFRMEEAIFLAHGSPSEKETEVPPFTEVYNNLNCMLLRCAPPNNGTHGS	538
C/Date: 10-Sep-1999 #sequence: G200216; revision 10-Sep-1999 #text_change 03-Jun-2002		C/Accession: A27410; I59055; S38354		Db	513	GSGPHGSQDNLFSNMOAFLFGYGAFFKIGAEVDSFENTEVYNNLNCMLLGLQPLAPNNGSGS	572
Rvan Driel, T.R.; Goding, J.W.		J. Biol. Chem. 262, 4882-4887, 1987		Qy	539	LNHHLKVPYEPHAEEVSKFSVCGFANPLPTESLDCPCPHLONSTOLEQDNOMNLTOE	598
A/Title: Plasma cell membrane glycoprotein PC-1. Primary structure deduced from cDNA c1c		A/Reference number: A27410; MUID:87165905; PMID:3104326		Db	573	LNLHLLKKPYPNPKPNSHKEFGFLSQC---PIKTSNSDLGCTCDPWIWPKDFKQLNLTE	628
A/Accession: A27410		A/Molecule type: mRNA		Qy	599	EITATVKVNLPFGRPRVILQKNDHCLLYTREYVSGFGKAMRVEWMSSYTVPLQGDTSFLP	658
A/Residues: 1-905 <VAN>		A/Cross-references: GB:J02700; NID:G200216; PID:9200237		Db	629	D-DDYRHMVTPYGGDRILKQHNVCLQQQFPLTGSYLDLMLPLWASTYF-LRNDQFSR	685
A/Note: The authors transcribed the codon CAG for residue 24 as Glu		A/Note: Authors: Wilkins, A.F.; Pietersz, G.A.; Goding, J.W.		Qy	659	PTVPPDCLRADVRYRPPSESOKCSFYLADKNTITHGFLYPPASNRTSDSOY-DALITSNLVPM	717
Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985		Proc. Natl. Acad. Sci. U.S.A. 82, 8619-8623, 1985		Db	686	DDFSNCMYPDLRIPSPVRCSTYKNSKLSYGFLPPPLRNYSNHTISEALLTSNIVPM	745
A/Title: Murine plasma cell membrane antigen PC-1: Molecular cloning of cDNA and analysis		A/Reference number: I59055; MUID:87165905; PMID:3104326		Qy	718	YEEFPKMDYFHSVLLKHTATERNGVNTYSGPLFDYNYDGHEDAPDEITKH--LANTDV	774
A/Accession: I59055		A/Status: preliminary		Db	746	YQSFQVWVYLHDTLILQYTAHERNGINVSGPVEDFDYGRDSLEIUKQNSVIRSOI	805
A/Molecule type: translated from GB/EMBL/DDJB		A/Residues: 203-219 <RES>		Qy	775	PIPTYFVWLTSCKNKSHTPENCGWLDLPLFTIPLHRPNVESCPGKPEALWTERFTA	834
A/Cross-references: GB:MI12552; NID:G200234; PID:9200235		A/Cross-references: GB:MI12552; NID:G200234; PID:9200235		Db	806	LIPPFPIVLTSCKOLSEPLECSA-LESSAYLPHRNNTESCHGREGSSVATEELTL	864
R.Belli, S.; van Driel, T.R.; Goding, J.W.		R.Belli, S.; van Driel, T.R.; Goding, J.W.		Qy	835	HIARYRVDVEILTGLFYQDKVQPVSEIQLQKTYLPTF	871
Eur. J. Biochem. 217, 421-428, 1993		Eur. J. Biochem. 217, 421-428, 1993		Db	865	HRARYRVDVEILTGLSFYQDQESVSEELLRKTHLPIF	901
A/Title: Identification and characterization of a soluble form of the plasma cell membrane		A/Title: Identification and characterization of a soluble form of the plasma cell membrane		RESULT 4			
A/Reference number: S38354; MUID:94039066; PMID:8223581		A/Reference number: S38354; MUID:94039066; PMID:8223581		A55453			
A/Accession: S38354		A/Status: preliminary		N/Contains: nucleotide diphosphatase (EC 3.6.1.9) - rat			
A/Molecule type: DNA		A/Molecule type: DNA		C/Species: Rattus norvegicus (Norway rat)			
A/Cross-references: GB:MI126; Domain: somatomedin B homology <SBH2>		A/Cross-references: GB:MI126; Domain: somatomedin B homology <SBH2>		C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002			
F161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted		F161,267,323,459,567,624/Binding site: carbohydrate (Asn) (covalent) #status predicted		C/Accession: A55453; JU0187			
F238/Binding site: AMP (Thr) (covalent) #status predicted		F238/Binding site: AMP (Thr) (covalent) #status predicted		R.Narita, M.; Goji, J.; Nakamura, H.; Sano, K.			
Query Match Score 50.2%; Best Local Similarity 50.7%; Pred. No. 7.9e-16; Matches 445; Conservative 152; Mismatches 251; Indels 29; Gaps 10;		J. Biol. Chem. 269, 2823-2842, 1994		A/Description: Cloning and expression of brain-specific phosphodiesterase			
Qy	10	EQPVKK-----NLUKVKIACVILVLLVMSLGLGLGKRLKQGSKKKCF	59	A/Title: Molecular cloning, expression, and localization of a brain-specific phosphodiesterase			
Db	39	EEPLEKADGARPAKDPT---YKWLSTLAVSVCLTTLGCIFLKPSCAKEVSKCRCF	95	A/Reference number: A55453; MUID:95050005; PMID:7961762			
Qy	60	DASFRGLENRGRCVADKQDGDCWDFFDTCVBSSTRWNCNPKCGETLEASLCSCDC	119	A/Molecule type: mRNA			
Db	96	ERTF---SNQRCDAACVCSGNCCDFQETCVPHEKVKCFCGEKRSRVCSCADD	152	A/Residues: 1-85 (NAR>			
Qy	120	LQKEDCCADYKSVCOGETSWLEENCDTAQOSOCREGFLPPVILFSMGGFRAYLYWT	179	A/Residues: 1-66, 'Q', 68-81, 'T', 83-94, 'C', 96, 'A', 98-195, 'A', 197-514, 'E', 516-621, 'E', 623-6			
Db	153	KTHNDCCINTSSVCDKSKSWEETESTDTPCPEAFFFSPPTILSFLGFRAYLHTGG	212	A/Experimental source: strain Sprague-Dawley			
Qy	180	IMPNNKLUKGCGHSKVMRAMPKTFPHYITVGLPESHGIDNNMYDYNLNQKNSFL	239	R.Narita, M.; Goji, J.; Nakamura, H.			
Db	213	LLPVSKLKNCGTGTNKRPMYPTKTFPHYSITVGLPESHGIDNNMYDPKNASSFL	272	C/Supfamily: nucleotide pyrophosphatase; somatomedin B homology			
Qy	240	SSKEQNNPAWHQDMWLTAMYQGLKAKATYWPPOSEWAINGSPSPSIYMPYNSVPPFERI	299	C/Keywords: coenzyme A; exonuclease; glycoprotein; phosphoprotein; phosphoric diester hy			
Db	273	KSKEKFNPLWYKGPQIWTWPAHPEVYKTSQGYFWPSDVEIDGIPDIXVYNGSVPPFERI	332	F:54-97/Domain: somatomedin B homology <SBH2>			
Qy				F:98-141/Domain: somatomedin B homology <SBH2>			
Db				F:53,150,316,405,522,608,829/Binding site: carbohydrate (Asn) (covalent) #status predicted			
Qy				F:207/Binding site: AMP (Thr) (covalent) #status predicted			
Db				Query Match	42.5%; Score 2043.5%; DB 1; Length 885;		

Best Local Similarity 41.7%; Pred. No. 6.8e-135; Indels 79; Gaps 12; Matches 380; Conservative 178; Mismatches 275; Amino acid sequence: KRNLLKKYIACIVLALLIVMSIGLGLGLRKLEK-----QGSC 54

Qy 14 RQCGLGSPFQVLSLTFAL----SYNICLGETASRIKAWDGGPTVTLSDSWNTNSGSC 58

Db 3 RKCEDDASSPGLENCRDVAACKDRGDCCDWFBDTCVSETRIMCNKFRGEIRLEASLCS 114

Qy 55 CSDDGLQKEDCCADYKSVQGETSWLNECDTAQQSOCOPBEGFDL--PPVTFMSMDGFRAE 118

Db 59 KGRCFELQVGPPDCRDNCKSYSSCCDDEBLCLTKVGECTDRSGEVRENEACH 114

Qy 115 A; Accession: A55144; A; Residues: 1-915 <MUR>

Db A; Cross-references: GB:J35594; NID:9537905; PID:AA64785.1; PID:9537905

Qy A; Note: Parts of this sequence were confirmed by peptide sequencing

Db R; Stracke, M.L.; Krutzsch, H.C.; Unsworth, B.J.; Arestad, A.; Cioce, V.; Schiffmann, E.; J. Biol. Chem. 269, 30419-30484, 1994

Qy A; Title: Cloning of the human tumor motility-stimulating protein, autotaxin, reveal a DNA sequence analysis of autotaxin, a novel

Db A; Reference number: A55144; MUID:95074054; PMID:7962964

Qy A; Molecule type: protein

Db A; Accession: A43239; MUID:92129337; PMID:1733949

Qy A; Molecular type: protein

Db A; Accession: A43239

Qy A; Gene: GDB:ATX

Db A; Cross-references: GDB:378346

Qy A; Map position: 8622-8676

Db A; Experiments: A2058 melanoma cells

Qy C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology

Db C; Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase

Qy F; 55-98/Domain: somatomedin B homology <SSH1>

Db A; Note: a peptide fragment Tyr-Asp-Val-Pro-Tyr-Asn-Glu-Thr-116 was also found

Qy C; Comment: This protein acts as an autocrine factor to stimulate tumor cell motility.

Db C; Genetics:

Qy A; Accession: A43239

Db A; Map position: 8622-8676

Qy A; Experiments: A2058 melanoma cells

Db A; Experiments: A2058 melanoma cells

Qy C; Superfamily: nucleotide pyrophosphatase; somatomedin B homology

Db C; Keywords: EF hand; glycoprotein; phosphoprotein; phosphoric diester hydrolase

Qy F; 99-142/Domain: somatomedin B homology <SSH2>

Db F; 54-463; 577-859/Binding site: AMP (Thr) (covalent) #status predicted

Db P; 210/Binding site: AMP (Thr) (covalent) #status predicted

Query Match 42.5%; Score 2040.5; DB 1; Length 915;

Best Local Similarity 40.5%; Pred. No. 1.2e-135;

Matches 379; Conservative 177; Mismatches 268; Indels 111; Gaps 11;

Qy 24 ACIVLLAVINSIGLGLGLRKLER-----QGSCKKCPDASF 63

Db 9 SCQISLTFAVGSVICHGFTAHRIKAEGWEGPPTVLSDSPWTNISGSCKGRCPELQE 68

Qy 64 RGCLENCFDVAKKDQGCGCWDPECTCUSTEIRWMCKFRGCGTRIASLCSQDDLGQRK 123

Db 69 AGPBDCCDNLCKSYTSCHDDELCIKTARGWECKDRCGEVRNEACHSEDCLARG 128

Qy 124 DCCADYKVSQCGETSWLJENCDTAQQQCPEFDLPPVILESMDGPRAEIYTWDTLMNP 183

Db 129 DCCTNQYQVCKESEHWDDEBEIKAECPAGEVRLPLIISVQDGRASMYKGSKMPN 188

Qy 184 INFLEKTCIHSKYMRYNPTKTFPNTYITVGLYPHESHGIDNNNNYDVNINKNFSLSKE 243

Db 189 TEKLRCGTHSPMMPYPTKTFPNLYTLATGLYPHSGHIVGNSMDPVFDTAFHLRGRE 248

Qy 244 QNNPANTWQGPKWMLTAMYQGLKAATYFWPGSEVAINGSFSPIYMPYNSYFPEERLSTLJ 303

Db 249 KENHRWGGQPWITATRQGKAGTFWW-----SIVPH-----ERRITIL 290

Qy 304 KWDLPLKAERPRFYTMYFEEPDSSGCHAAGGPPVSA-----

Db 251 RWTLPDHERPSVYAFSSEQPDPSGKHYQGPGEPESSYGSFTPAKPKRKVAKRQER 350

Qy 337 -----RVIKAQVVDIAFGMLMEGLKQRNLHNCVNLILLA 371

Db 351 PVAPPKCRRKLRKTHRDHYAETRQDMTNPLREIUKVQGLMDGKQLKLRRCVIVFVG 410

Qy 372 DHGMDQTYCNRKEMYDIFPSINFFMVEGAPRIR--AHNIPHDFFSFNSEEIVRNLS 428

Db 411 DHGMDYTCRDTFEELSNVLTNVDDITLVPGLGRSRKSFNNAKYD----PKAIIANLT 465

Qy 429 CRKPDPDFKPKLTPDLPKRLHYAKNVRDRKVLFLYDQW----LAVRSKSNTNC-GGG 481

Db 466 CKKPDPDFKPKLQKLPKRLHYANRRIEDIHLVERWVARKPLDVKKPSGKCFQG 525

RESULT 5

A55144

autotaxin precursor - human

N; Contains: phosphodiesterase I (EC 3.1.4.1)

C; Species: Homo sapiens (man)

Query 482 NFGYNNPFRSMEAIFIAGPSRFKEXTTEVEPPENIVYNNACDLRIOPAPNGHFGSLNH 541
 Database 526 DHGFDNKVNNSMGTQFVYGYGPFKVKVPPENIELYNNCKDLGKPKAPNGHFGSLNH 585

Query 542 LLRVPPFVPSHABEVSKPSVCCFANPLPTESLDCFC- PHILONSTOLEQNONMLNLTQEEI 600
 Database 586 LIRNTNTPPTMBEVTRNPYPPIMYQSDFDIGCTDDKYEPKNNLDELNKRHTK--- 641

Query 601 TATVKVNLIFGRPRVLRQNDHCLLYTREYVSGFKAMRPMWSSYTVPLQGDTSPPLPT 660
 Database 642 GSTEERHLLYGRPAVLX-TRYDILYHTDPESGYSEIFLMLWTSVTSRQAEVSSVDPH 700

Query 661 VPDCLRADVRYPSESEOKCSPTYADNTLTSNLYPMYEE 720
 Database 701 LISCVRPPRVRSPSFSONCLAVKNDKOMSYGTLFPYLSSEPEAKYDAFLYTNKPMYPA 760

Query 721 FKKWQDWFHVSLLIKHATERGNYVNSGPIFDYNYQGHDFADEDEIKHLANTDVP1PTHY 780
 Database 761 FKKWQDWFHVSLLIKHATERGNYVNSGPIFDYNYQGHDFADEDEIKHLANTDVP1PTHY 820

Query 781 FVVLTSCKNSHTPENCGWLDLPPFLPHRPTNVEKSCPEAKWEEERTTAHYAVR 840
 Database 821 YSLITSCUDFTQPADKCGPLSYSSFTPHRDNEESCSSEDESKRVEELMKHHTAVR 880

Query 841 DVEILTGGDFYQDKVQPSRSPSYPEILTKTLYLHTYESBI 875
 Database 881 DIBHTSLDFFRKTSRSYSPPEILTKTLYLHTYESBI 915

RESULT 6

Query 931 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4.
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Accession: T0931 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
 A;Reference number: T0931
 A;Genetics: ATSP: T16L4.190
 A;Map position: 4
 A;Cross-references: EMBL: AL079344; GSDDB: GN00062; ATSP: T16L4.190
 C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match 15.4%; Score 743.5; DB: 2; Length 496;
 Best Local Similarity 41.0%; Pred. No. 1.4e-44;
 Matches 159; Conservative 71; Mismatches 141; Indels 17; Gaps 9;

Query 157 DLPPVILFMDGDFRAEYLWTDIMPNNKLKGIGIHSKY-MRAMYPPKTKPENHYTTWG 215
 Database 105 DKPVVLLISSDGFR--FGQFQKTKLPSHRLIANGTEATGLPVFPLTFPHYSITWG 162

Query 216 LYPSHGGIDDNMYDNLNQFNSLSSKSEQNNPNAWQHGPMLWAMYQGKAAATYFWPSE 275
 Database 163 LYPAHGIIINHNFVDPETGNVFTMASHE---PEWNLGEPIWETVNGQGKAAATYFWPSE 219

Query 276 WAINGSF---PSIYMPYNGSVPFPEERSTIILKWDLPLRAERPRYTMFPEEPDPSGHKG 332
 Database 220 VH-KGWNCPGLCONYNGSVPFDDVDTIISYFPLPNEIPEMSMTLVEPDPHQHVG 278

Query 333 PVSARYTKALQVVDHAFGMMEGLKQRNLHNCVNNTLADHGMQDTCNKMEXMTDYPR 392
 Database 279 PDDPQTEAVNNIDRJGRGLDGLERGIFDVTMVGPHGMVTCDRKLVVLDDAW 338

Query 393 INF---FYMFGPAPRRAHNIPHDESENSEEIVNLSORKPD--QHFKPVLTPDLPKR 447
 Database 339 IKIPSSWVQYTTPLAIOPPS-GHDAADIV-A-KINEGLSSGKVENGVKLVKLVLDLPSR 396

Query 448 LYAKNVNRIDKVLFVDOQMLAVRSKENTNCQGGNHYNNERPSMEAIFIAGPSFKEKT 507
 Database 397 LYVDSDRIPPIGLVDEGEKYBOKSKAKEGGAHYDNAAFSMRTTIFGHGMPMSKGR 456

Query 508 EVEPENIEVNYNLMCLLRIOPAPNGT 535
 Database 457 KVPSFENQIYNTSISLGLKAPNNGS 484

RESULT 7
 T0333 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) - ric
 C.Species: Oryza sativa (rice)
 C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Aug-2002
 C;Accession: T03233
 A;Description: Rice early embryogenesis gene.
 A;Reference number: Z14889
 A;Accession: T03293
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-47 HSI>
 A;Cross-references: EMBL: U25430; NID: 9818848; PID: 9818849
 A;Experimental source: strain Tatnung 67
 C;Genetics:
 C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4
 C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase

Query Match 15.4%; Score 737.5; DB: 2; Length 479;
 Best Local Similarity 42.0%; Pred. No. 3.4e-44;
 Matches 163; Conservative 64; Mismatches 140; Indels 21; Gaps 10;

Query 159 PPVILFMSMDGFRAEYLWTDIMPNNKLKGIGIHSKY-MRAMYPPKTKPENHYTTWG 217
 Database 90 PVVILISSDGRFGQHRAAT--PHIRLIGNTGTSATGLVPIFPLTFBNHYSATGLY 147

Query 218 PESHGIDDNMYDYNKNSKLNKNSLSSKEQNNPDAWQHGPMLTAMYCGLKZATYFWGSEVA 277
 Database 148 PSSHGIDTINNYPDPISGDYFTMSSHE--PKWNLGEPWLNATAODGIAQATYFWGSEVK 204

Query 278 INGSF--PSIY-MPINGSVPFEEERSTIILKWDLISKAERPRYTMFPEEDSSGHAGGPV 334
 Database 205 -KGSDWCDPKYCRHNTGVPFEEERYDAILGYFDLPSDEMQLFLTYFEDDQHGVQPD 263

Query 325 SARVTKALQVVDHAFGMMEGLKQRNLHNCVNNTLADHGMQDTCNKMEXMTDYPRIN 394
 Database 264 DPAITEAVRVIDEMIGRLIAGLEERGVFEDDVNLVGDHGMVCTDKKLVFLDELAPWIK 323

Query 395 F---FYMFGPAPRRAHNIPHDESENSEEIVNLSORKPD--QHFKPVLTPDLPKR 447
 Database 324 LBEDWVLSMTPLLAIR---PPDDMSLPDVVAKMNEGLGSKVNGEYRLMYLKDLPQR 379

Query 448 LYHAKNVNRIDKVLFVDOQMLAVRSKENTNCQGGNHYNNERPSMEAIFIAGPSFKEKT 507
 Database 380 LYHADSTRIPPIGLPPEGYKEMRSKDNKGAGHYDNAFFSMTTIFAHGPRFEGGR 439

Query 508 EVEPENIEVNYNLMCLLRIOPAPNGT 535
 Database 440 VVPSFENQIYNTSISLGLKAPNNGS 467

RESULT 8
 T0932 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Accession: T0932 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
 A;Reference: R.Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Newes, H.W.; Mayer, K.F.; submitted to the Protein Sequence Database, June 1999
 A;Reference number: 216897
 A;Accession: T0932

A;Molecule type: DNA	Db	58	PVTLIMISCDGFRFGYQEKDTD--PNIDLISGGTEAKHGLIIPVFPPTMTPNHYISATGHL 115
A;Residues: 1-457 <BEV>	Qy	218	PESHGIDDNMMYDVLNKNQFSLSSKEQNNDPAWHEGQPMWLTAMYQGLKATYFPGSEVA 277
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .200	Db	116	PAYHGIMNKPTIDPVGEVNKGLO--PKWNLGEPLWVTAQNQGLKAVTYFPGSEVA 171
C;Experimental source: cultivar Columbia; BAC clone T16L4	Qy	278	ING-SEPSIAMP-INGSVPEERESTLKLWLDLKAERFRFTYMFEEBDSSGHAGGPVS 335
C;Genetics:	Db	172	KSSWTCPBGICPHENLUSVPLEERVDSVLSHFDLLEDEVDLMLYFDEPDQSHNYGDD 231
A;Gene: ATSP:T16L4 .200	Qy	336	ARTVAKLQVVDHAFGLMELKQNLHNCVNTILADHOM-DQTYCNKMEYNTDYPFRI 393
A;Map position: 4	Db	232	PRVTAVSVRVDKMRVKGKLOKQREIFDEVHVLIGDHMVNTCNEKAVIYDLDW1 291
C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4	Qy	394	NFFYMYEGPAPRRAHNIPHDFFFSNSE-----EVRLNSCR-----KPDQ 434
C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase	Db	292	KI-----PAWICAYS--PVLAIPONGKDVENOSSENAEVAKMNEALSSGGKVNGE 342
Query Match	Qy	407	PNHTIVTGVYEPSEHGLDNNMMYDVLNKNFSLSSKEONPAAWHGQPMWLTAMYQGLK 266
Best Local Similarity 38.5%; Pred. No. 1.9e-42;	Db	102	PNHFSIATGQYPAHGIIMKTFDPVSGELFN--RNLPKRWLGPBLWTAQNQGLMA 157
Matches 166; Conservative 76; Mismatches 144; Indels 41; Gaps 12;	Qy	2677	ATYWPAGSVAINGSF--PSIY--MPYNGSVPEERESTLKLWLDLKAERFRFTYMF 322
Score 712.5; DB 2; Length 457;	Db	158	ATYWPAGDVH-KCSWNCFKGFCRAPTNSVPEERDTILNLYFDLPERE.FDPMALYFD 216
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	322	EPDSSGHAGGPVSARVTKLQVVDHAFGLMELKQNLHNCVNTILADHGMQDTCNK 382
Matches 166; Conservative 76; Mismatches 144; Indels 41; Gaps 12;	Db	211	EPDITQHGBYGPDPDPRVTAISKVQDKGTRINGLEKRVFSQDYLDEGMVTCNK 276
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	363	MEYMTDYFPRINFFYMYEGPAPRRAHNIPHDFFFSN--SBEIVRN-- 426
Score 14.8%; Score 712.5; DB 2; Length 457;	Db	277	VTIDDLAWIKI-----PAWICAYS--PVLAIPONGKDVENOSSENAEVAKMNEALSSGGKVNGE 327
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	427	-LSCRK--PDQHKPKVLTDLPLPKRLHYAKNVRIDKVLFDQQLAVRSKSNTNCGGNH 483
Score 14.8%; Score 712.5; DB 2; Length 457;	Db	328	AUSSGKVANGEFQVQLKENLQRHLYSDDSSRIPPIIYGEGLAKYKCNRYVQECSGH 387
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	484	GINNEFRNEAIFIHLAHDPSFKEKTEVEVNLMDLRLQAPAPNTHGSLNHL 543
Score 14.8%; Score 712.5; DB 2; Length 457;	Db	388	GYDNMFMSRS1EVGYGPRFRGKVSFENTQVNAEFLGLRPAPNGSSLTRSL 447
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	544	KVBFYERSHAE 554
Score 14.8%; Score 712.5; DB 2; Length 457;	Db	448	-LPFGERTSQVE 457
RESULT 9			
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	T0933	Probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4 .
C;Species: Arabidopsis thaliana (mouse-ear cress)	Db	Db	C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Aug-2002
C;Accession: T0933	Qy	Db	R;Bevan, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
A;Reference number: Z16897	Db	Qy	R;Submitted to the protein Sequence Database, June 1999
A;Molecule type: DNA	Db	Db	A;Accession: T0933
A;Residues: 1-461 <BEV>	Qy	Db	A;Experimental source: cultivar Columbia; BAC clone T16L4
A;Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4 .210	Db	Qy	A;Genes: ATSP:T16L4 .210
C;Genetics:	Db	Db	A;Map position: 4
C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase 4	Qy	Db	C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase
Query Match	Qy	14.2%; Score 680.5; DB 2; Length 461;	
Best Local Similarity 38.7%; Pred. No. 3.4e-40;	Db	Qy	14.2%; Score 680.5; DB 2; Length 461;
Matches 155; Conservative 70; Mismatches 137; Indels 39; Gaps 11;	Qy	Db	14.2%; Score 680.5; DB 2; Length 461;
Score 14.8%; Score 712.5; DB 2; Length 457;	Qy	159	PPVILFSMDGGERAEIYLWTMLPNIKURTCGHHSKY-MRAVYPTKTFPHYTTIVGHL 217

Db	299	EEIPERNHYKHNDRVQPIVAADEGWLQNKSD-DFLGLNGYDYNALAEHMPIFLAHGP	357	submitted to the EMBL Data Library, September 1999
Qy	502	SFREKTEVEPPENIEVTLNLMCDLRLIQDAPANGTHGSNLHLIKVPPSHAEVNSKFSV	561	A; Description: Contains actin, gamma pseudogene 9, a gene similar to PLASMA-CELL MEMBRAN
Db	358	AFFKNEFTEAMNTDLYSLIUCHNLNLPHNGSEWVQDLI-----	399	A; Reference number: A59391
Db	562	CGFANPLPIESLDCFCPLQNSTQL	586	A; Molecule type: DNA
Qy	400	-SSATPKP-----IPTQSTRL	416	A; Residues: 1-477 <SMA>
Db	400	-SSATPKP-----IPTQSTRL	416	A; Cross-references: GB:AU035701; NID:5924007; PIDN:CA56566.1
RESULT 11				
Qy	14657	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9)	SPBC72	R; Gijsbers, R.; Cellemans, H.; Stalmans, W.; Bollen, M.
C;Species:	Schizosaccharomyces pombe			J. Biol. Chem. 276: 1361-1368, 2001
C;Date:	03-Dec-1999	#sequence_revision 03-Dec-1999	#text_change 16-Aug-2002	A; Title: Structural and catalytic similarities between nucleotide pyrophosphatases/phos
C;Accession:	T40657			A; Reference number: A59390; MUID:1125673; PMID:11027689
A;Status:	translated from GB/EMBL/DBJ			A; Contents: annotation
A;Molecule type:	DNA			C;Genetics:
A;Residues:	1-485 <LYN>			A;Gene: ENPP5
A;Cross-references:	ENBL:AL034352; PIDN:CAA22177.1; GSPDB:GN00067; SPDB:SPBC725.05C			A;Map position: 6011.2-6P21.1
A;Experimental source:	strain 972h-; cosmid c725			C;Superfamily: human phosphodiesterase I / nucleotide pyrophosphatase
C;Genetics:	SPDB:SPBC725.05C			C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase
A;Map position:	2			F;72/Active site: Thr #status predicted
C;Superfamily:	human phosphodiesterase I / nucleotide pyrophosphatase			Query Match
C;Keywords:	A; metalloprotein; phosphoric diester hydrolase			13 2%; Score 632.5; DB 1; Length 477;
Query	161	VILFSMDGFRAEIYLTWDTLMPINKLNKLGTCGTHSKYMLAMYPIKTFPHYTTVTGLYPS	220	Best Local Similarity
Db	76	VIVISLDGFRAIDLRYGFT--PNLSSLARENTHVPPFLPSFSITFPHYTTVTGLYPS	133	34 4%; Pred. No. 4.2e-37;
Qy	221	HGTIDNNMVDVNLINKFNSLSSKEON-NPAWM-HGQPMVMTANTOGKKAATYFWPGSEVAI	278	Matches 146; Conservative
Db	134	HGIYVSNFFNDFDPTVKGQFQNSMPECNKDPTWWDQGPBPIVNAEUNVSAVHWPGNVEN	193	14 6%; Mismatches 165; Indels 14; Gaps 8;
Qy	279	NGSPPSIIMPYNGSVPFPEERIYSTLKLWDLPKAERPRPYTMYFEEPDSSGHAGGPYSARV	338	Qy
Db	194	HGYRPTYSDFGDNFTDTLREKDKDRLWDLDPDKDREQLLATAVPHDMVGHAFGPDSPEL	253	13.3%; Score 637; DB 2; Length 485;
Qy	339	IKALOVIDHAFGMLMEGLKORNLLNCVNTILLADHGMQTYCNKMTTDYPRINFYM	398	Db
Db	254	NIIQEVNDIVIGELJEGLKRNTDKHVNUTIFLSHGMWAPTSNDRLNDNMNLSAYHR	313	13.7%; Pred. No. 4.2e-35;
Qy	399	YEGPAPRRAHNIPHDFFSNSEEIVRLNLSCKRKPD-QHFKPYLTPDLKRLHYAKNVID	457	Qy
Db	314	DAWPLGGFRRGSESDLDDEYY--ESLVNYSRSSLPSAENWVNTSKKDIFSRWHYNNERIA	371	12.9%; Score 636; DB 2; Length 485;
Qy	458	KVHLFVDFQWMLAV---RSKSNTNCGGNGYNNFRSMEAFLAHLGPFSK--EKTEVEP	511	Db
Db	372	PVMMIPDVGMSLVSMLDHSPELEYEPLGVYGDNLSPNRAFLTAGSSFKNFKGKLLAP	431	12.9%; Pred. No. 4.2e-35;
Qy	512	FENIEVYNNLMDLRLIQPAPNNGTH-GSL	539	Qy
Db	432	FQNTIYGLSHLDPQPNNGTYEGAL	460	12.9%; Pred. No. 4.2e-35;
RESULT 12				
A5931	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9)			A; Experimental source: liver
N;Alternate names:	ectonucleotide pyrophosphatase/phosphodiesterase 5; NPP5			R; Oda, Y.; Kuo, M.D.; Huang, S.S.; Huang, J.S.
C;Species:	Homo sapiens (man)			J. Biol. Chem. 268: 27318-27326, 1993
C;Date:	18-Jul-2001	#sequence_revision 18-Jul-2001	#text_change 16-Aug-2002	A; Title: The major acidic fibroblast growth factor (aFGF) - stimulated phosphoprotein from esterase activities
C;Accession:	A59391			A; Reference number: A49308; MUID:1715869
R;Smalley, C.				A; Accession: A49308; PMID:7505270

A;Accession: B59391
A;Molecule type: DNA
A;Residues: 1-453 >SMA>
A;Cross-references: GB:AU035701; NID:95924008; PIDN:CAB56567.1
C;Keywords: coenzyme A; metalloprotein; phosphoric diester hyd
C;Genetics:
A;Gene: ENPP4

Query	Match	Score	Length	DB	1;
Best Local Matches	Similarity	35.5%;	Pred. No.	1.3e-36;	
Matches 139;	Conservative	76;	Mismatches	153;	Indels 23;
158 LPP-VTLESMQDFRAEYLYTDTLMPPNINKLKTGHSKYMBAAMYPTKTFPNHYTTITGGL	216				
24 LPPKLILVSEDFRADYLKNNK--FPHLQNFTEKGVLVEHVKRNFLKTFPHYSYTGGL	81				
217 YPESHSGLIYDNMNYDNMANKNFLSSEQNNPAWHA-GQPMWLT-ATYQGLKATYTFPGS	274				
82 YEESHGIVANSMYDAYTKKHSFDSN--DKDPFWNNEAVPIWTNQLOQNRSAAAAMPGT	139				
275 EVAINGSFPSIYMPYNGSVPPFERIRSTIILKWLDPKAERP-RFYTMYFEEDPSGHHAGGP	333				
140 DVPIHDITSSYFMMYNSSVSFERLNNTMWN--NSNPPVTATLWEEPDASGHKYGP	197				
334 V-SARYVIKALQYVDHAFGMLMEGLKQRNLHNCVNIILLADHGMQDTQNCMXYMTDYPFR	392				
QY	198 EDKENNSRVLKCKDIDLQYRLKMLGLWENLNIVVITSDHMTQCSQDRLINLSDCTIDH	257			
Db	393 INFYYNTEGPAPIRAHNIPHDFFSINSEEIVRNLSRKPDQHFKP11TPDLPKRHYAK	452			
Qy	258 SYYTLDSLPSVAAI---LP---KINRTEVYNNKLKNCSP--HMNVYK1KEDIPNRYFYYQH	307			
Db	453 NVRIDKVLHFLYDQOWLAVRSKSNTNCGGGNHGYNNFRSMEATFLAHCPSFKEKTEVEPF	512			
Qy	308 NDRIQPIILVADGWTIVLNBSQKL--GDHGVDNSLPSMHPFLAAGPAFKGYKESTI	365			
Db	513 ENIEVNLNCMLIRIOPAPNNTGHSLNHLI	543			
Qy	366 NIVDIPNMCHLIGLKHDPHNNNGFQHTKCLL	396			
Db					

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